

FIGURE 1

CGGACGCGTGGGTGCGAGGCCAAGGTGACCGGGGACCGAGCATTTTCAGATCTGCTCGGTAGA
 CCTGGGTGCACCAACCACCATGTTGGCTGCAAGGCTGGTGTGTCTCCGGACACTACCTTCTAGG
 GTTTTCCACCCAGCTTTCCACCAAGGCCCTCCCTGTTGTGAAGAAATCCATCAGCAAGAATCA
 ATGGCTGTTAAACACCTAGCAGGGAATATGCCACCAAAACAAGAATTTGGGATCCGGCGTGGGA
 GAACTGGCCAAGAAGCTCAAAGAGGCAGCATTTGGAACCATCGATGGAAAAAATATTTAAAT
 GATCAGATGGGAAGATGGTTTGTGCTGGAGGGGCTGCTGTTGGTCTTGGAGCATTGTGCTA
 CTATGGCTTGGGACTGTCTAATGAGATTGGAGCTATTGAAAAGGCTGTAATTTGGCCTCAGT
 ATGTCAAGGATAGAATTCATTCACCTATATGTACTTAGCAGGGAGTATTGGTTTAAACAGCT
 TTGTCTGCCATAGCAATCAGCAGAACGCCTGTTCTCATGAACTTCATGATGAGAGGCTCTTG
 GGTGACAATTGGTGTGACCTTTGCAGCCATGGTTGGAGCTGGAATGCTGGTACGATCAATAC
 CATATGACCAGAGCCCAGGCCAAAGCATCTTGCTTGGTTGCTACATTCTGGTGTGATGGGT
 GCAGTGGTGGCTCCTCTGACAATATTAGGGGGTCTCTTCTCATCAGAGCTGCATGGTACAC
 AGCTGGCATTGTGGGAGGCCTCTCCACTGTGGCCATGTGTGCGCCAGTGAAAAGTTTCTGA
 ACATGGGTGCACCCCTGGGAGTGGGCCTGGGTCTCGTCTTTGTGTCCTCATTGGGATCTATG
 TTTCTTCCACCTACCACCGTGGCTGGTGGCCACTCTTTACTCAGTGGCAATGTACGGTGGATT
 AGTTCCTTTTCAGCATGTTCTTCTGTATGATACCCAGAAAGTAATCAAGCGTGCAGAAGTAT
 CACCAATGTATGGAGTTCAAAAATATGATCCCATTAACTCGATGCTGAGTATCTACATGGAT
 ACATTAATATATTTATGCGAGTTGCAACTATGCTGGCAACTGGAGGCAACAGAAAAGAAATG
 AAGTGACTCAGCTTCTGGCTTCTCTGTACATCAAATATCTTGTTTAAATGGGCGAGATATGC
 ATTAATAATGTTTGTACAGACAGCTTTCGTTGAAGTTTGAAGATAAGAAACATGTCTCATATA
 TTTAAATGTTCCGGTAAATGTGATGCCTCAGGTCTGCCTTTTTTTCTGGAGAATAAATGCAGT
 AATCCTCTCCCAATAAGCACACACATTTTCAATTTCTCATGTTTGAGTGATTTTAAATGTT
 TTGGTGAATGTGAAAACATAAGTTTGTGTGATGAGAATGTAAGTCTTTTTTCTACTTTAAAA
 TTTAGTAGGTTCACTGAGTAACATAAAATTTAGCAAACTGTGTTTGCATATTTTTTTGGAGT
 GCAGAATATTGTAATTAATGTCATAAGTGATTTGGAGCTTTGGTAAAGGACAGAGAGAAG
 GAGTCACCTGCAGTCTTTTGTTTTTTAAATACTTAGAACTTAGCACTTGTTGTTATTGATTA
 GTGAGGAGCCAGTAAGAAACATCTGGGTATTTGGAACAAGTGGTCATTGTTACATTCATT
 GCTGAACCTTAACAAAACGTTCATCCTGAAACAGGCACAGGTGATGCATCTCTGCTGTTG
 CTTCTCAGTGCTCTCTTCCAATATAGATGTGGTCATGTTGACTTGTACAGAATGTTAATC
 ATACAGAGAATCCTGTGGAATTATATATGTGTGTTTTACTTTTTGAATGTTACAAAAGGAA
 ATAACCTTAAAACTATTCTCAAGAGAAAATATTCAAAGCATGAAATATGTTGCTTTTTCCAG
 AATACAAACAGTATACATG

FIGURE 2

MLAARLVCLRTLPSRVFHPAFTKASPVVKNSITKNQWLLTPSREYATKTRIGIRRGRTGQEL
KEAALEPSMEKIFKIDQMGRWFVAGGAAVGLGALCYGLGLSNEIGAIEKAVIWPQYVKDRI
HSTYMYLAGSIGLTALSAIAISRTFVLMNFMMRGSWVTIGVTFAAMVGAGMLVRSIPYDQSP
GPKHLAWLLHSGVMGAVVAPLTLGGPLLIRAAWYTAGIVGGLSTVAMCAPSEKFLNMGAPL
GVGLGLVFVSSLGSMFLPPTTVAGATLYSVAMYGGLVLFMSFLLYDTQKVIKRAEVSPMYGV
QKYDPINSMLSIYMDTLNIFMRVATMLATGGNRKK

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FIGURE 3

GAAGGCTGCCTCGCTGGTCCGAATTCCGGTGGCGCCACGTCGCGCCGCTCTCCGCCTTCTGCAT
 CGCGGCTTCGGCGGCTTCCACCTAGACACCTAACAGTCGCGGAGCGCGCGCGCTCGTGAGGG
 GTTTCGGCAGCGGGAGTCGGGCGGTCTTGTGCATCTTGGCTACCTGTGGTCCGAAGATGTCGG
 ACATCGGAGACTGGTTCAGGAGCATCCCGCGCATCACGCGCTATTGGTTTCGGCGCCACCGTC
 GCCGTGCCCTTGGTCGGCAAACTCGGCCCTCATCAGCCCGCCCTACCTCTTCCCTCTGCCCCGA
 AGCCTTCCTTTATCGCTTTCAGATTTGGAGGCCAATCACTGCCACCTTTTATTTCCCTGTGG
 GTCAGGAACCTGGATTTCTTTATTTGGTCAATTTATATTTCTATATCAGTATCTCAGCGCA
 CTTGAACAGGAGCTTTTGTATGGGAGGCCAGCAGACTATTTATTCATGCTCCTCTTTAACTG
 TGTCACTACCTTATGCTGGGCCAGCTGAACAGAGACATGATGATCATTTTGGTTTGGAG
 ACACGATTTAAGGCTGCTATTTACCTGGGTTATCCTTGGATTCAACTATATCATCGGAGG
 CTCGGTAATCAATGAGCTTATTGGAATCTGGTTGGACATCTTTATTTTTCTTAATGTTCA
 GATACCCAATGGACTTGGGAGGAGAAATTTCTATCCACACCTCAGTTTTTGTACCGCTGG
 CTGCCCAGTAGGAGAGGAGGAGTATCAGGATTTGGTGTGCCCCCTGCTAGCATGAGCGGAG
 TGCTGATCAGAAATGGCGGAGGCGGAGACACAACCTGGGCCCAGGGCTTTCGACTTGGAGACC
 AGTGAAGGGGCGGCCCTCGGCGAGCCGCTCCTCTCAAGCCACATTTCTCCAGTGCTGGGGT
 CACTTAACAACCTGCGTTCTGGCTAACACTGTGGACCTGACCCACACTGAATGTAGTCTTTT
 AGTACGAGACAAGTTTCTTAAATCCCGAAGAAAAATATAAGTGTTCCACAAGTTTACAGAT
 TCTCATTTCAGTCCCTTACTGCTGTGAAGAACAATAACCACTGTGCAAAATGTGCAAACTGAC
 TACATTTTGGTGTCTTCTCTCTCCCTTTCCGCTGAATAATGGGTTTTCAGCGGTCCT
 AATCTGCTGGCATTGAGCTGGGGCTGGGTACCAAACCTTCCCAAAGGACCTTATCTCTT
 TCTTGACACATGCTCTCTCCCACTTTTCCCAACCCCACTATTTGCAACTAGAAAAAGTTG
 CCATATAAATGCTCTGCCCTTGACAGGTTCTGTTATTTATTGACTTTTGCAAGGCTGGT
 ACAACAATCATATTACGTTATTTCCCTTTTGGTGGCAGAACTGTACCAATAGGGGGAG
 AAGACGCCAGCGATGAAGCGTTTCTCAGCTTTTGGAAATGCTTCGACTGACATCCGTTGTT
 AAGCGTTTGGCACTCTCAGATATTTTTATAAAAAAAGTACCACTGAGTTTATGAGGGCCA
 CAGATTTGGTTATTAATGAGATACGAGGTTGGTGCTGGGTGTTGTTTCTGAGCTAAGTGA
 TCAAGACTGTAGTGGAGTTGCAGCTAACATGGGTTAGGTTTAAACCATGGGGGATGCACCCC
 TTTGCGTTTCATATGAGCCCTACTGGCTTGTGTAGCTGGAGTAGTTGGGTTGCTTTGTGT
 TAGGAGGATCAGATCATGTTGGCTACAGGAGATGCTCCTTTGAGAGGTCCTGGGCATG
 ATTCCCATTTCAATCTCATTCTGGATATGTGTTCAATTGAGTAAAGGAGGAGACCCCTATA
 CGCTATTTAAATGTCACTTTTTTGCCCTATCCCCCGTTTTTGGTTCATGTTTCAATTAATTGT
 GAGGAAGGCGCAGCTCCTCTCTGCACGTAGATCATTTTTTAAAGCTAATGTAAGCACATCTA
 AGGGAATAACATGATTTAAGGTTGAATGGCTTTAGAATCATTTGGGTTTGGGGTGTGTTA
 TTTTGAGTCATGAATGTACAAGCTCTGTAATCAGACAGCTTAAATGAAACACCTTTTTT
 TCGTAGTGGGCTTTTCTATCAGAGCTTGGCTCATAACCAATAAAGTTTTTTGAAGGCCA
 TGCTTTTTCACACAGTTATTTTTATTTATGACGTTATCTGAAAGCAGACTGTTAGGAGCAGT
 ATTGAGTGGCTGTCACTTTTGGGCAACTAAAAAGGCTTCAACAGTTTGTATCAGTTTCTT
 TTCAGGAACATTGTGCTCAACAGTATGACTATTTCTTCCCCACTCTTAAACAGTGTGAT
 GTGTGTTATCCTAGGAAATGAGAGTTGGCAAACAACCTTCTCATTTTGAATAGAGTTTGTGTG
 TACTCTCCATATTTAATTATATGATAAAATAGGTGGGAGAGCTGAACCTTAACTGTCA
 TGTTTTGTGTTTCATCTGTGGCCACAATAAAGTTTACTTGTAAAAATTTAGAGGCCATTACT
 CCAATTATGTTGCAGTACACTCATTTGACAGGCGTGAGACTCATGTATGTATAAGAATA
 TTTCTGACAGTGAGTGACCCGAGTCTCTGGTGTACCTCTTACAGCTGAGCTGCTGCGAG
 CAGTCATTTTCTTAAAGGTTTACAAGTATTTAGAATTTTCACTTCAGGCGAAAATGTTCT
 ATGAAGTTATTTCTCTTAAACATGGTTAGGAAGCTGTAGAGTTATTTGATTTTGTCTGGAT
 ATGTTTCTGGAATAATTTTACCAAAACAAGCTATTTGAGTTTTGACTTGACAAGGCAAAACA
 TGACAGTGGATTCTCTTTACAAATGAAAAAAAATCTTATTTTGTATGAAGGACTTCCC
 TTTTGTGAACATAATCTTTTATTTGGTAAAAATGTAAATTTAAATGTCAACTG

FIGURE 4

MSDIGDWFRSIPAITRYWFAATVAVPLVGKLGGLISPAYLFLWPEAFLYRFQIWRPITATFYF
PVGPGTGFLYLVNLYFLYQYSTRLETGAFDGRPADYLFMLLFNWICIVITGLAMDMQLLMIP
LIMSVLYVWAQLNRDMIVSFWFGTRFKACYLPWVILGFNYIIGGSVINELIGNLVGHLYFFL
MFRYPMDLGGRNFLSTPQFLYRWLPSRRGGVSGFGVPPASMRRAADQNGGGGRHNWGQGFRL
GDQ

Transmembrane domain:

amino acids 98-116, 152-172

N-myristoylation site.

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

Glycosaminoglycan attachment site.

amino acids 218-222

FIGURE 5

GGGGCCGCGGTCTAGGGCGGCTACGTGTGTTGCCATAGCGACCATTTTGCATTAACTGGTTG
 GTAGCTTCTATCCTGGGGGCTGAGCGACTGCGGGCCAGCTCTTCCCTACTCCCTCTCGGGT
 CCTTGTTGGCCCAAAGGCCTAACCGGGTCCGGCGGTCTGGCCTAGGGATCTTCCCGTTGCC
 CCTTTGGGGCGG**CAT**GGCTGCGGAAGAAGAAGACGAGGTGGAGTGGGTAGTGGAGAGCATCG
 CGGGGTTCCTGCGAGGGCCAGACTGGTCCATCCCCATCTTGGACTTTGTGGAACAGAAATGT
 GAAGTTAACTGCAAAGGAGGGCATGTGATAACTCCAGGAAGCCCAGAGCCGGTGATTTTGGT
 GGCCTGTGTTCCCTTGTTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGATTC
 ATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTTGGAATT
 AATGAAGATCAATTTCAAGAAGCATGCACCTCTCCTCTTGCAAAGACCCATACATCACAGGC
 CATTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCCAGA
 AAAACATTGAAATGCAGCTGCAAGCCATTTCGAATAATTCAAGAGAGAAATGGTGTATTACCT
 GACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAATCCT
 GAGGGAAGTTCTTAGAAAATCAAAGAGGAATATGACCAGGAAGAAGAAAGGAAGAGGAAAA
 AACAGTTATCAGAGGGCTAAAACAGAAGAGCCACAGTGCATTCCAGTGAAGCTGCAATAATG
 AATAATTTCCCAAGGGGATGGTGAACATTTTGACACCCACCCTCAGAAGTTAAATGCATTT
 TGCTAATCAGTCAATAGAACCTTTGGGAAGAAAAGTGGAAAGTCTGAACTTCTCCCTCC
 CACAAAAGGCCTGAAGATTCTGGCTTAGAGCATGCGAGCATTGAAGGACCAATAGCAAAC
 TTATCAGTACTTGGAACAGAAGAACTTCGGCAACGAGAACACTATCTCAAGCAGAAGAGAGA
 TAAGTTGATGTCCATGAGAAAGGATATGAGGACTAAACAGATACAAAATATGGAGCAGAAAG
 GAAAACCCACTGGGGAGGTAGAGGAAATGACAGAGAAACCAGAAATGACAGCAGAGGAGAAG
 CAAACATTACTAAAGAGGAGATTGCTTGAGAGAAACTCAAAGAAGAAGTTATTAATAAG**TA**
ATAATTAAGAACAATTTAACAAAATGGAAGTTCAAATGTCTTAAAAATAAATTATTTAGTC
 CTTACACTG

FIGURE 6

MAAEEDEVEWVVESIAGFLRGPDWSIPLDFVEQKCEVNCKGGHVITPGSPPEFVILVACVP
LVFDDEEESKLTYTEIHQYKELVEKLLEGYLKEIGINEDQFQEACTSPLAKTHTSQAILQP
VLA AEDFTIFKAMMVQKN IEMQLQAIRIIQERNGLVPDCLTDGSDVVS DLEHEEMKILREVL
RKSKEEYDQEERKRKKQLSEAKTEEPTVHSSEAAIMNNSQGDGEHFAHPPSEVKMHFANQS
IEPLGRKVERSETSSLPQKGLKIPGLEHASIEGP IANLSVLGTEELRQREHYLKQKRDKLMS
MRKDMRTKQIQNMEQKGKPTGEVEEMTEKPEMTAE EKQTLKRRLLAEKLKEEVINK

N-glycosylation sites.

amino acids 224-228, 246-250, 285-289

N-myristoylation site.

amino acids 273-279

Amidation site.

amino acids 252-256

Cytosolic fatty-acid binding proteins.

amino acids 78-108

GGGCACAGCACATGTGAAGTTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGAT
TCATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGTTACCTCAAAGAAATTGGAA
TTAATGAAGATCAATTTCAAGAAGCATGCACCTTCTCCTCTTGCAAAGACCCATACATCACAG
GCCATTTTGCACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCC
AGAAAAACATGAAATGCAGCTGCAAGCCATTCAATAATTCAGAGAGAAAATGGTGTATTA
CTGACTGCTTAAACCGTGCCTGATGTGGTCAGTGCACCTTGGAACCGAAGATGAAAAAT
CCTGAGGGGAAGTTCTTAGAAATCAAAGAGGAATATGACCGAGAA

FIGURE 8

GCGTGGTTTTTGTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTTCGCCATACCTACTG
 TAGCTTCTCCACGTATGGACCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTG
 TCTCAGCTCTAGGATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATAAAAAAC
 AGTGGAAATGGAAAAACAGTGTGTAGTCACTGTAATATGCTCCTGTCAACAAGTATATAC
 ATTCTGTCTAGGTGCCATATTCTATTGCTTTAAGCTCAAGTCGCACTTACTAGTGAAGTAT
 CTGCCAATGAAGAAAAACAAGTATGATTATCTTCCAACACTGTGAATGTGTGCTCAAGACTG
 GTGAAGCTAGTTTTCTGTGTGCTTGTGTCATTCTGTGTTATAAAGAAAGATCATCAAAGTAG
 AAATTTGAAATATGCTTCTGGAAGGAATTTCTGTATTTCATGAAGTGGTCCATTCTGCCT
 TTTCTTTATTTCTCGGATAACTTGATTGCTCTCTATGCTCTGCTATCTTCAACAGCCATG
 GCTGTTATCTTCTCAAATTTTAGCATTATAACAACAGCTCTTCTATTTCAGGATAGTGTGAA
 GAGGCGTCTAAACTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTGTCTATTGTGGCCT
 TGACTGCCGGGACTAAACCTTTACAGCACAACTTGGCAGGACGTGGATTTCATCACGATGCC
 TTTTTCAGCCCTTCCAATTTCTGCCCTTCTTTTCAAGAGTGAAGTGTCCAGAAAAGACAATTG
 TACAGCAAAAGGAATGGACTTTTCTGAGCTAAATGGAACACCACAGCCAGAGTTTTCAGTC
 ACATCCGCTCTGGCATGGGCCATGTTCTTATTATAGTCCAGTGTTTTTATTCTTCAATGGCT
 AATATCTATAATGAAAGATACCTGAAGGAGGGGAACACAGCTCACTGAAAGCATCTTCATACA
 GAACAGCAACTCTATTCTTTGGCATTCTGTTTAAATGGGCTGACTCTGGGCCCTTCAGAGGA
 GTAACCGTGATCAGATTAAGAACTGTGGATTTTTTTATGGCCACAGTGCATTTTCAGTAGCC
 CTATTATTTGTAAGTGCATTCCAGGGCCTTTCAGTGGCTTTCATTCTGAAGTTCCTGGATAA
 CATGTTCCATGCTCTGATGGCCAGGTTACCAGCTGCTATTATCAACAAGTGTCTGTCTGG
 TCTTTGACTTCAGGCCCTCCCTGGAATTTTTCTTGGAAAGCCCCACTCAGTCCCTCTCTATA
 TTTATTTATAATGCCAGCAAGCTCAAGTTCGGAATACGCCAATAGGCAAGAAAGGATCCG
 AGATCTAAGTGGCAATCTTTGGGAGCGTTCAGTGGGGATGGAGAAGAACTAGAAAGACTTA
 CCAAAACCAAGAGTGATGAGTCAGATGAAGATACTTTCTAACTGGTACCCACATAGTTTGCA
 GCTCTCTTGAACCTTATTTTCACTTTTCAGTGTGTTGTAATATTTATCTTTTCACTTTGATA
 AACCAGAAATGTTTCTAAATCCTAATATCTTTGCATATATCTAGCTACTCCCTAAATGGTT
 CCATCCAAGGCTTAGAGTACCCAAAGGCTAAGAAATTCATAAGAACTGATACAGGAGTAACA
 ATATGAAGAATTCATTAATATCTCAGTACTTGATAAATCAGAAAGTTATATGTGCAGATTAT
 TTTCTTGGCCCTTCAAGCTTCCAAAAAATTTGTAATAATCATGTAGCTATAGCTTGTATAT
 ACACATAGAGATCAATTTGCCAAATATTCACAATCATGTAGTCTGATTACATGCCAAAGT
 CTCCCTTTTAAACATATAAAGCTAGGTTGTCTCTTGAATTTTGAAGGCCCTAGAGATAGT
 CATTTTGAAGTAAAGAGCAACGGGACCCTTCTAAAAACGTTGGTTGAAGGACCTAAATAC
 CTGGCCATACCATAGATTTTGGGATGATGTAGTCTGTGCTAAATATTTTGTGGAAGACGAGT
 TTCTCAGACACAACATCTCAGAATTTTAATTTTGAATTCATGGGAATTTGGATTTTGT
 AATAATCTTTGATGTTTTAAACATTGGTTCCCTAGTCACCATAGTTACCACTTGTATTTA
 AGTCATTTAAACAAGCCAGGTTGGGCTTTTTTCTCCTCAGTTTGAGGAGAAAAATCTTGAT
 GTCAATCTCTGAATTTATACATTTTGGAGAATAAGAGGGCACTTTTATTTATAGTTACT
 AATTCAAGCTGTGACTATTGTATATCTTCCAAGAGTTGAATGCTGGCTTCAAGCATAC
 CAGATTTGTGAGTGTGATGCTTAGGAATTTTAAAGGGATCCTTTCAAAGGATCACTT
 AGCAAAACACATGTTGACTTTTAACTGATGTATGAATATTAATCTCTAAAAATGAAAGAGC
 AGTAAATATAAGTCACTTTACAGTGCTACTTCACACTTAAAGTGGATGGATTTTTCATG
 GTATTTTGCATGCAAGCAGTTAACTCTCGTAGATAGAGAAGTCAGGTGATAGATGATATAA
 AAATTAAGCAAAACAAAGTGACTTGCTCAGGGTCATGCAGCTGGGTGATGATAGAAGTGGG
 CTTTAACTGGCAGGCTGTATGTTTACAGACTACCATGATAAATAGAGCTTTATGGTGT
 CATCTCAGAAACTTATACATTTCTGCTCTCCTTTCTCCTAAGTTTCATGCAGATGAATATA
 AGGTAATATACTATTATAATCTATTGTATCCCAATAATATGACTGGCAAGAAATG
 GTGGAATTTGTAATTAATAATTTAAACCT

FIGURE 9

MEKQCCSHPVICSLSTMYTFLLGAIFIALSSSRILLVKYSANEENKYDYLPTTVNVCSELVK
 LVFCVLVSFCVIKKDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLQPAMAV
 IFSNFSIITALLFRIVLKRRLNWIQWASLLTLFLSIVALTAGTKTLQHNLAGRGFHHDADF
 SPSNSCLLFRSECPRKDNTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISSMANI
 YNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRSNRDQIKNCGFFYGHSAFSVALI
 FVTAFAQGLSVAFILKFLDNMFHVLMAQVTTVIIITVSVLVFDFRPSLEFFLEAPSVLLSIFI
 YNASKPQVPEYAPRQERIRDLSGNLWERSSSGDGEELERLTKPKSDESDETF

Transmembrane domains:

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293,
 298-318, 328-368

N-glycosylation sites.

amino acids 128-132, 204-208, 218-222, 374-378

Glycosaminoglycan attachment site.

amino acids 402-406

N-myristoylation sites.

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

FIGURE 10

CGTGCCTGCGCAATGGGTGTCGGGTCCGCTTTTTCCCAATCCGGACGTAATCGTGGTTTTTG
TTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTCGCCTATACCTACTGTAGCTTCTCCAC
GTATGGACCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAG
GATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTAAAAACAGTGGAATGGAA
AAACAGTGCTGTAGTCATCCTGTAATATGCTCCTTGCAACAATGTATACATTCTGCTAGG
TGCCATATTCAATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATTCTGCCAATGAAG
AAAACAAGTATGATTATCTTCCAACACTGTGAATGTGTGCTCAGAACTGGTGAAGCTAGTT
TTCTGTGTGCTTGTGTCATTCTGTGTTATAAAGAAAAGATCATCAAGTAGAAATTTGAAATA
TGCTTCCTGGAAGGAATTCTCTGATTTTCATGAAGTGGTCCATTCTGCCTTTCITTTATTTCC
TGGATAACTTGATTGCTTCTATGTCCTGTCTTCTTCAACCAGCCATGGCTGTTATCTTC
TCAAATTTTAGCATTTATAACAACAGCTCTTCTATTTCAGGATAGTGCTGAAGAGGCGTCTAAA
CTGGATCCAGTGGGCTTCCTCTGACTTTATTTTTGTCTATTGTGGCCTTGACTGCCGGGA
CTAAAACTTTA

FIGURE 11

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGCGGCTTGGCTAGCGCGCGGCGGCC
 GTGGCTAAGGCTGCTACGAAGCGAGCTTGGGAGGAGCAGCGGCCCTGCGGGGCGAGAGGAGCAT
 CCCGCTACCAAGGTCCCAGCGGCGTGGCCCGCGGGTTCATGGCCAAAGGAGAAGGCGCCGAG
 AGCGGCTCCGCGGCGGGGCTGCTACCCACCAGCATCCTCCAAAGCACTGAACGCGCGGCCCA
 GGTGAAGAAAGAACCGAAAAAGAAACAACAGTTGCTGTGTTGCAACAAGCTTTGCTATG
 CACTTGGGGGAGCCCCCTACCAGGTACGGGCTGTGCCCTGGGTTTCTTCCTTCAGATCTAC
 CTATTGG**ATGT**GGGCTCAGGTGGGCCCTTTCTCTGCCCTCCATCATCCTGTTTGTGGGCGGAGC
 CTGGGATGCCATCAGAGCCCTCGTGGGCGCTCTGCATCAGCAAATCCCCCTGGACCTGCC
 TGGGTCGCCTTATGCCCTGGATCATCTTCTCCACGCCCCGCGCTATTGCCTACTTCTCT
 ATCTGGTTCGTGCCGACTTCCCACAGCGCCAGACCTATTGGTACCTGCTTTTCTATTGCCT
 CTTTGAACAATGGTCACGTGTTTCCATGTTCCCTACTCGGCTCTCACCATTGTTTCATCAGCA
 ACCGAGCAGACTGAGCGGGATTCTGCCACCGCCTATCGGATGACTGTGGAAGTGCTGGGCAC
 AGTGCTGGGCACGGCGATCCAGGGACAATCGTGGGCCAAGCAGACACGCCTTGTTTCCAGG
 ACTTCAATAGCTCTACAGTAGCTTCACAAAGTGCCAACCATACACATGGCACCCTTCACAG
 AGGGAACGCAAAAGGCATACCTGCTGGCAGCGGGGTCATTGCTGTATCTATATAATCTG
 TGCTGTCTATCCTGATCCTGGGCGTGGCGGAGCAGAGAAACCTATGAAGCCAGCAGTCTG
 AGCCAATCGCCTACTTCCGGGGCCTACGGCTGGTCATGAGCCACGGCCCATACATCAAATT
 ATTACTGGCTTCCTCTTACCTCCTTGGCTTTTATGCTGGTGGAGGGGAACCTTTGCTCTGTT
 TTGCACCTACACCTTGGGCTTCCGCAATGAATCCAGAAATCTACTCCTGGCCATCATGCTCT
 CGGCCACTTTAACCATTTCCCATCTGGCAGTGTTTCTTGACCCGGTTTGGCAAGAAGCAGCT
 GTATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAA
 CCTCATATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCCTTCTTAC
 TACCCTGGTCCATGTGCTGCTGATGTGCTATTGACGACTTCCATCTGAAGCAGCCCCACTTCCAT
 GGAACCGAGCCCATCTTCTCTCTTCTATGTCTTCTTCCACCAAGTTTGCCCTCTGGAGTGTC
 ACTGGGCACTTTCTACCCTCAGTCTGGACTTGCAGGGTACCAGACCCGTGGCTGCTCGCAGC
 CGGAACGTGTCAAGTTTACACTGAACATGCTCGTGACCATGGCTCCCATAGTTTCTCATCCTG
 CTGGGCTGCTGCTCTTCAAATGTACCCCATTTGATGAGGAGAGGCGCGGCGAGAATAAGAA
 GGCCCTGCAGGCACTGAGGGACGAGGCCAGCAGCTCTGGCTGCTCAGAAACAGACTCCACAG
 AGCTGGCTAGCATCCTCT**AG**GGGCGCGCCACGTTGCCCGAAGCCACCATGCAGAAGGCCACAG
 AAGGGATCAGGACCTGTCTGCCGGCTTGCTGAGCAGCTGGACTGCAGGTGCTAGGAAGGGAA
 CTGAAGACTCAAGGAGGTGGCCAGGACACTTGCTGTGCTCACTGTGGGGCGGCTGCTCTG
 TGCCCTCCTGCTTCCCTCTGCCTGCTGTGGGCGCAAGCCCTGGGGCTGCCACTGTGAATA
 TGGCAAGGACTGATCGGGCTAGCCGGAACACTAATGTAGAAACCTTTTTTTTACAGAGCC
 TAATTAATACTTAATGACTGTGTACATAGCAATGTGTGTATGTATATGTCTGTGAGCTA
 TTAATGTTATTAATTTTCATAAAAGCTGGAAGC

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGCGGCTTGGCTAGCGCGCGGCGGCC

MWLRWALS LPPSSCLWAE PGMPSQT PWWASAS ANPPGPAWVALCPGSSSPRPWPSLPTSSSG
SCPTSH TARPIGTCF SIASLQKQSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVLGTVL
GTAIQQGQIVGQADTPCFQDFNSSTVASQSANHTHGTTHSHRETQKAYLLAAGVIVCIYIICAV
ILILGVREQREPEYEAQQSEPIAYFRGLRLVM SHGPYIKLITGFLTSLAFMLVEGNFVLFCT
YTLGFRNEFQNLLA IMLSATLTIPIQWFLTRFGKKTAVYVGISSAVPFLILVALMESNLI
ITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHGTEPIFFSFYVFVFTKFASGVSLG
ISTSLSDFAGYQTRGCSQPERVKFTLNLMLVTMAPIVLILLGLLLFKMYPIDEERRQNKKAL
QALRDEASSGCSCTSDTELASIL

FIGURE 13

GGGAAACGCAAAGGCATACCTGCTGGCAGCGGGGGTCATTGTCTGTATCTATATAATCTGT
GCTGTCATCCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCTATGAAGCCCAGCAGTCTGA
GCCAATCGCCTACTTCCGGGGCCTACGGCTGGTCATGAGCCACGGCCCATACATCAAACCTTA
TTACTGGCTTCCTCTTACCTCCTTGGCTTTCATGCTGGTGGAGGGGAACCTTGTCTTGTTT
TGCACCTACACCTTGGGCTTCCGCAATGAATTCCAGAATCTACTCCTGGCCATCATGCTCTC
GGCCACTTTAACCATTCCCATCTGGCAGTGGTTCTTGACCCGGTTTGGCAAGAAGACAGCTG
TATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAAC
CTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTACT
ACCCTGGTCCATGCTGCCTGATGTATTGACGACTTCCATCTGAAGCAGCCCCACTTCCATG
GAACCGAGCCCAT

FIGURE 14

GGGGCTTCGGCGCCAGCGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGT
ATGAGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAACAGAAAACCTGTTAGAAATGT
GGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCT
TTCATATTTTCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATAT
CAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGG
CAGTTTTATGCATTGCTACCATTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAA
GAGAACGTTATCATCAAATTAACAAGGCTGGCCTTGACTTGGAATACTGAGTTGTTTAGG
ACTTTCATTGTGGCAAACCTCCAGAAAACAACCTTTTGTCTGCACATGTAAGTGGAGCTG
TGCTTACCTTTGGTATGGGCTCATTATATATGTTTGTTCAGACCATCCTTTCCTACCAAATG
CAGCCCAAATCCATGGCAAACAAGTCTTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGG
AGTAAGTGCACCTTAGCATGCTGACTTGCTCATCAGTTTGTGACAGTGGCAATTTTGGGACTG
ATTTAGAACGAAACTCCATTGGAACCCCGAGGACAAAGGTTATGTGCTTCACATGATCACT
ACTGCAGCAGAATGGTCTATGTCATTTTCCTTCTTTGGTTTTTTCCTGACTTACATTCGTGA
TTTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACATGGATTAACCTCTATGACACTG
CACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCAGAGATATTTGATGAAAGGAT
AAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGGTTACAGAAAGTTGCTTA
TTCTTCTCTGAAATTTCAACCACTTAATCAAGGCTGACAGTAACACTGATGAATGCTGATA
ATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTTCTAAAGGATATCATCAAGAAGACTA
TTAAAAACACCTATGCCTATACTTTTTTATCTCAGAAAAATAAAGTCAAAAGACTATG

FIGURE 15

MWWFQQGLSFLPSALVIWTSAAFI¹FSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNI
AAVLCIATIIYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSG
AVLTFMGSLYMFVQ²TILSYQM³QPKIHGKQVFWIRLLLLVIWCGVSALSMLTCSSVLHSGNFG
TDLEQKLHWNPEDKGYVLHMITTA⁴AEWSMSFS⁵SFFGFFLYIRDFQKISLRVEANLHGLTLYD
TAPCPINNERTRL⁶LSRDI

T04111-4440660

FIGURE 16

CGGACGCTTGGGCNCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGTGCCTGATGCCGAGT
TCCGTCTCTCGGGTCTTTTCCTGGTCCCAGGCAAAGCGGAGCGGAGATCCTCAAACGGCCTA
GTGCTTCGCGCTTCCGGAGAAAATCAGCGGTCTAATTAATTCCTCTGGTTGTTGAAGCAGT
TACCAAGAATCTTCAACCCCTTCCCAAAAAGCTAATTGAGTACACGTTCCCTGTTGAGTACA
CGTTCCTGTTGATTTACAAAAGGTGCAGGTATGAGCAGGTCTGAAGACTAACATTTTGTGAA
GTTGTA AACAGAAAACCTGTTAGAAATGTGGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCT
TCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTTTCATACATTACTGCAGTAACACT
CCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGGTACAGTANC

FIGURE 17

CCCACGCGTCCGCCCGCCGCTGCGTCCCGAGTGCAAGTGAGCTTCTCGGCTGCCCCGCGGG
 CCGGGGTGCGGAGCCGACATGCGCCCGCTTCTCGGCCTCCTTCTGGTCTTCGCCGGGTGCAC
 CTTTCGCTTGTACTTGTGTCGACGCGACTGCCCGCGGGCGGAGACTGGGCTCCACCGAGG
 AGGCTGGAGGAGGTGCTGTGGTTCCCCCTCCGACCTGGCAGAGCTGCGGGAGCTCTCTGAG
 GTCCTTCGAGAGTACCGGAAGGAGCACCAGGCCTACGTGTTCTGCTCTTCTGCGGCGCCTA
 CCTCTACAAACAGGGCTTTGCCATCCCCGGCTCCAGCTTCTGAAATGTTTTAGCTGGTGCCT
 TGTTTTGGGCCATGGCTGGGGCTTCTGCTGTGCTGTGTGTTGACCTCGGTGGGTGCCACATGC
 TGCTACCTGCTCTCCAGTATTTTTGGCAAACAGTTGGTGGTGTCTTACTTCTCTGATAAAGT
 GGCCCTGCTGCAGAGAAAGGTGGAGGAGAACAGAAACAGCTGTGTTTTTTTCTTATTGTTTT
 TGAGACTTTTCCCATGACACCAAAGTGGTTCCTGAACCTCTCGGCCCAATTCTGAACATT
 CCCATCGTGCAGTTCTTCTCTCAGTTCTTATCGGTTTGATCCCATATAAATTCATCTGTGT
 GCAGACAGGGTCCATCCTGTCAACCTTAACCTCTCTGGATGCTCTTTTCTCCTGGGACACTG
 TCTTTAAGCTGTTGGCCATTGCCATGGTGGCATTAAATTCCTGGAACCCCTCATTAAAAAATTT
 AGTCAGAAACATCTGCAATTGAATGAAACAAGTACTGCTAATCATATACAGTAGAAAAGA
 CACATTGACTCGGATTTTCTGTTTGCCACATCCCTGGACTCAGTTGCTTATTTGTGTAATGGA
 TGTGGTCCCTAAAGCCCCCTCATTGTTTTGATTGCCTTCTATAGGTGATGTGGACACTGTG
 CATCAATGTGCAGTGTCTTTTCAGAAAGGACACTCTGCTCTTGAAGGTGATTACATCAGGT
 TTTCAAACCAGCCCTGGTGTAGCAGACACTGCAACAGATGCCTCCTAGAAAAATGCTGTTTGT
 GGCCGGGCGCGGTGGCTCAGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCCGGTGATTTC
 ACAAGGTGAGGAGTTCAAGACCAGCCTGGCCAAGATGGTGAAATCCTGTCTCTAATAAAAAAT
 ACAAAAAATTAGCCAGGCGTGGTGGCAGGCACCTGTAATCCAGCTACTCGGGAGGCTGAGGC
 AGGAGAAATTGCTTGAACCAAGGTGGCAGAGGTTGAGTAAGCCAAGATCACACCCTGCACT
 CCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

FIGURE 18

MRPLLGLLLVFAGCTFALYLLSTRLPGRRLGSTEEAGGRSLWFPSPDLAEELRESEVLREYR
KEHQAYVLLFCGAYLYKQGFAPGSSFLNVLAGALFGPWLGLLLCCVLTSVGATCCYLLSS
IFGKQLVVSYPDPKVALLRKVEENRNSLFFFLFLRLFPMTNWFNLNSAPILNIPIVQFF
FSLVIGLIPYNFICVQTGSILSTLSTLDALFSWDTVFKLLAIAMVALIPTGLIKKFSQKHLQ
LNETASNIHHSKDT

Important features:

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 101-123, 189-211

N-glycosylation sites.

amino acids 172-176, 250-254

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 240-244, 261-265

N-myristoylation site.

amino acids 13-19, 104-110, 115-121, 204-210

Amidation site.

amino acids 27-31

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 4-15

Protein splicing proteins.

amino acids 25-31.

Sugar transport proteins.

amino acids 162-172

FIGURE 19

CCGAGGCGGGAGGAGCCCCGAGGGGGCGCGAGCCCCGCATGAATCATTGTAGTCAATCATTTT
 CCAGTTCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTCCGAACTGCCAGCTCAGAA
 TAGGAAAATAAATTGGGATTTTATATTGGAAGAC**ATG**GATCTTGCTGCCAACGAGATCAGCA
 TTTATGACAACTTTTCAGAGACTGTTGATTGGTGAGACAGACCGGCCATCAGTGTGGCATG
 TCAGAGAAGGCAATTGAAAAATTTATCAGACAGCTGCTGGAAGAATGAACCTCAGAGACC
 CCCCCGCAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCT
 TGCTCACTGCCTACTTTGTGATTCAACCTTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTCT
 GGAGCTCACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCCTTGCCCATTGCCAA
 GAAGTACATGTCAGAAAATAAGGGAGTTCCTCTGCATGGGGGTGATGAAGACAGACCCCTTTC
 CAGACTTTGACCCCTGGTGGACAAACGACTGTGAGCAGAATGAGTCAGAGCCCATTCCTGCC
 AACTGCAGTGGCTGTGCCAGAAACACCTGAAGGTGATGCTCCTGGAAGACGCCCCAAGGAA
 ATTTGAGAGGCTCCATCCACTGGTGATCAAGACGGGAAAGCCCTGTTGGAGGAAGAGATTTC
 AGCATTTTTTGTGCCAGTACCCTGAGGCGACAGAAGGCTTCTGTAAGGGTTTTTCGCCAAG
 TGGTGGCGCTGCTTTCCTGAGCGGTGGTCCCATTTCCTTATCCATGGAGGAGACCTCTGAA
 CAGATCACAAATGTTACGTGAGCTTTTCCTGTTTTCACTCACCTGCCATTTCCAAAAGATG
 CCTCTTTAAACAAGTGCTCCTTTCTTCACCCAGAACCTGTTGTGGGGAGTAAGATGCATAAG
 ATGCCTGACCTATTTATCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTTCCA
 GTGCCGAAGACATTGTAGTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTCTG
 ACACCACCACTGGAAGGTCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTTCATCTGCGAT
 GGAACCGCTTTCTCAGAAGT**CTAG**GAAATAGAACTGTGCACAGGAACAGCTTCAGAGCCGA
 AAACCAGGTTGAAAGGGGAAAAATAAAAACAAAACGATGAAACTGCAAAA

MDLAANEISIDYDKLSETVDLVRQTGHQCGMSEKATEKFIQRLLEKNEFQRPFPQYPLLIVVY
KVLATLGLILLTAYFVIQPFSEPLAPEPVLGSAHTWRSLLHHIRLMSLP IAKYMSENKGVPL
HGGDEDRPFPDFDPWWTNDCEQNESEPIPANCTGCAQKHLKVMLLEDAPRKFERLHPLVIKT
GKPLLEEEIQHFLCQYPEATEGVFSEGFFAKWWRFCWFRWFFPYWRRRLNRSQMLRELFPV
FTHLPFPKDALSNKCSFLHPEFVGVGSKMKHMKDLFTIGSGEAMLQLPFPFQCRRHCQSVAMP
IEPGDIGYDSTLTHHWKVIARGVQVPLICDTAFSEL

FIGURE 21

CCACGGTGTC CGTTCTTCGCCCCGGCGGCAGCTGTCCCCGAGGCGGGAGGAGCCCCGAGGGGCG
CGAGCCCCGCATGAATCATTGTAGTCAATCATTTTCCAGTTCTCAGCCGTT CAGTTGTGATC
AAGGGACACGTGGTTTCCGAAC TGCCAGCTCAGAATAGGAAAATAACTTGGGATTTTATATT
GGAAGACATGGATCTTGCTGCCAACGAGATCAGCATTTATGACAAACTTT CAGAGACTGTTG
ATTTGGTGAGACAGACCGGCCATCAGTGTGGCATGT CAGAGAAGGCAATTGAAAAATTTATC
AGACAGCTGCTGAAAAAGAATGAACCTCAGAGACCCCCCGCAGTATCCTCTCCTTATAGT
TGTGTATAAGGTTC TCGCAACCTTGGGATTAATCTTGCTCACTGCCTACTTTGTGATTCAAC
CTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTGTGGAGCTCAC

FIGURE 22

CCCACGCGTCCGCCACGCGTCCGGCTGAACACCTCTTCTTTGGAGTCAGCCACTGATGAGG
 CAGGGTCCCCACTTGCAGCTGCAGCAGCTGCAGCAGCTGCAGAGCGCTGCTCTGGCTGGTG
 CCATGGTGGCAGCGTCTAGACCGTGCTATGAGCCGTGGGCGTGCAGTGGGGACTGCC
 CTCCCTGCCACCCCAATGGCAGCCCCACCTTCTTTGAAGACTTCCAGGCTTTTGTGCCA
 CACCCGAATTGGCGCCACTTTCATCGACAAACAGGTACAGCCAACCAATGCCAGTTCGAAATG
 GACACGTATGCTAAGAGGCCACGACCTTATGTGAGTTTCTGGAATGCCGTCTATGACATGCT
 TATGACAGTGGGGCAGCGCGCCAGTGGGAGCGCGCCAGAGTCGTCTGGGCGCTTCCAGGAGC
 TGGTGCTGGAACCTGCGCAGAGGCGGGCGCGCTGGAGGGGTACGCTACACGGCAGTGCTG
 AAGCAGCGCAACGCGAGCACTCCATGGCCCTGCTGCACTGGGGGGCGCTGTGGCGCCAGCT
 CGCCAGCCCATGTGGGGCTGGGCGCTGAGGGACACTCCCATCCCCCGCTGGAACATGTCCA
 GCGCCGAGACATATTACGCAATGCGTCTGAAGCTGGTGCCCAACCATCACTTCGACCCCTCAC
 CTGGAAGCCAGCGCTCTCCGAGACAATCTGGGTGAGGTTCCCTGACACCCACGAGGAGGC
 CTCACCTGCTCTGGCAGTGACCAAGAGGCCAAAGTGAGCACCACCCGAGTTGCTGCAGG
 AGGACAGCTCGGCGAGGACGAGCTGGCTGAGCTGGAGACCCGATGGAGGCGAGCAAACTG
 GATGAGCAGCGTGAGAAGCTGGTGCTGTGCGCCGAGTGCCAGCTGGTGACGGTAGTGGCCGT
 GGTCCAGGGCTGCTGGAGGTACCACACAGAATGTATACTTCTACGATGGCAGCACTGAGC
 GCGTGGAAACCGAGGAGGCATCGGTATGATTTCCGGCGCCACTGGCCAGCTGGCTGAG
 GTCCACCTGCGCGCTTTCAACCTGCGCCGTTCAGCACTTGAGCTCTCTATTCTGATCAGGC
 CAACTACTTCTCAACTTCCATGCAAGGTGGGACGACCCAGCTCATCTCATCTATGCCAGA
 CTCGAGACCCCGAGCTGGCGCCATCCACCCCATACCCAGGTACGGAACCGAGGTGATCTG
 TGCTCTGCGCCCTACGGCCCCCTCTCAAGGCTACCTAAGCAGCCGCTCCCCAGGAGAT
 GCTGCGTGGCTCAGGCGTTACCCAGAAATGGGTACAGCGTGAGATATCCAACCTTCGAGTACT
 TGATGCAACTCAACACCATTTGCGGGCGGACCTCAATGACCTGTCTCAGTACCTGTGTTT
 CCCTGGGTCTGCGAGGACTACGTGTCCCCAACCTTGGACCTCAGCAACCCAGCGCTGTCCG
 GGAACCTGTAAAGCCTCGGTGTGGTGAACCCCAAGCATGGCCAGCTCGTGAGGAGAAAT
 ATGAAAGCTTTGAGGACCCAGCAGGGACATTGACAAGTTCCACTATGGCACCCCACTACTCC
 AATGCGCAGGCGTGATCCACTACTCTATCCGCGTGGAGCCCTTCACTCCCTCAGCTCCA
 GCTGCAAGATGGCCGCTTTGACTGCTCCGACCGGCACTTCCACTCGGTGGCGGAGCCTGGC
 AGGCACGCTGGAGAGCCCTGCCGATGTGAAGGAGCTCATCCCGAATTCTTACTTTCTT
 GACTTCTGGAGAACCAGAACCGTTTTGACCTGGGCTGTCTCCAGCTGACCAACGAGAAGGT
 AGGCGATGGTGCTTACCCCGTGGGCGAGCTCTCCTGAGGACTCATCCAGCAGCACCGCC
 AGGCTCTGGAGTCGGAGTATGTGCTGCAACCTTACACGAGTGGATCGACCTCATCTTTGGC
 TACAAGCAGCGGGGGCCAGCGCGCGAGGAGGCCCTCAATGTCTTCTATTACTGCACTATGA
 GGGGGCTGTAGACCTGGACCATGTGACAGATGAGCGGGAACGGAAGGCTCTGGAGGGCATTA
 TCAGCAACTTTGGGCAGACTCCTGTCACTGCTGAGTGGAAGGACCATCCAATCGGCTCTCA
 GCTTGAGGAAGCAGCCCATCGCTTGCAGCGCTGGACACTAATCACTACCTAGCATCTCCAGCA
 CTTGAGCAACTCAAGGCATTTCTGCGAGGTTGACTGTGAGTGCCAGTGGGCTGCTGGGCA
 CCCACAGCTGGTTGCCCTATGACCGCAACATAAGCACTACTTCACTTCAGCAAGAGCCCC
 ACCATGGGCGGCCACAAGACCGCAGCGACTGCTGAGTGGCCGTGGGTGCCAGGAGTGGTGT
 GAGTGGACAAGCACTGGCAGTGGCCCCGAGTGGAAAGCTGCTATTCAAGCGGTGGCCACTGGG
 ATGGCAGCTTGGGTGACTGCACTACCCGCTGGCAAGCTGTTGAGCCAGCTCAGCTGCCAC
 CTTGATGTAGTAACCTGCCTTGCACTGGACACTGTGGCATCTACCTCATCTCAGGCTCCCG
 GGACACCAAGCATGGTGTGGCGGCTCCTGCATCAGGCTGGCTGTGTGCTAGGCGCTGGCAC
 CAAAGCCTGTGCAGGTCTGTATGGGCGATGGGGCTGCAGTGAGCTGTGTGGCCATCAGCACT
 GAACCTGACATGCTGTGTCTGGATCTGAGGATGGAATGTGATCATACACTGTACGCGC
 CGGACAGTTTGTAGCGGCACTACGGCTCTGGGTGCCACATTCCTTGGACCTATTTTCCGCC
 TGGCATTTGGGTCCGAAGGCCAGATTGTGGTACAGAGCTCAGCGTGGGAACGCTCTTGGGGC
 CAGGTCACTACTCTTGCACCTGTATTGAGTCAATGGGAAGTTGGCGGCTTCACTGCCCCCT
 GGCAGAGCAGCTCATACGCGCTGACGGTGACAGGAGCTTTGTGTTGCTGGGACCCGCGAGT
 GCGCCCTGCACTACTCCAACATAACACACTGCTCCCGGCGCGCTCCTTGTGCCATGTGAAG
 GTGGCCATCCGACGCTGGCGTGACCAAGGAGCGCAGCCAGTGTGTTGGGCTGGAGGA
 TGGCAAGCTCATCTGTTGGTGGTCCGGGGGACGCGCTCTGAGGTGGCGAGCAGCCAGTCCGCG
 GGAAGCTGTGGCGGTGCTCGCGCGCACTTCCAGGTGTCTCGGAGAGACGGAATACAAC
 CCTACTGAGGCGCGCTGCAACTGGCCAGTCCGGCTGCTCGGGCCCGCGCCCGGCGAGCGCT
 GCGCGGAGGCGCCGCGCAAGTCCGCGGGGAACACCCGGGGTGGGACGCTCAGGGGTGA
 GCGGGGCCACCCCTGCCAGCTCAGGATTGGCGGGCATGTTACCCCTCAGGAGTTGGCG
 GCGGAAGTCCCGCGCTGCGCGGCTGAGGGCGCGCGTGAAGGCGAGCTGCGGCT

FIGURE 23

MSQFEMDITYAKSHDLMSGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLEPAQRRARLEGL
 RYTAVLKQQATQHSMLLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRKLKLPN
 HHFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDELAELETP
 MEAAELDEQREKLVLSAECQLVTVVAVVPGLLLEVTTQNVYFYDGGSTERVETEEGIGYDFRRP
 LAQLREVHLRRFNLRRSALELFFIDQANYFLNFPCKVGTTPVSSPSQTPRPQPGPIPPHTQV
 RNQVYSWLLRLRPSPQGYLSSRSPQEMLRASGLTQKWWQREISNFEYLMQLNTIAGRTYNDL
 SQYPVFPWVLQDYVSPPTLDLSNPAVFRDLSKPIGVVNPKHAQLVREKYESFEDPAGTIDKFH
 YGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDCSDRQFHSVAAAWQARLESPADVKEKIP
 EFFYFPDFLENQNGFDLGCLQLTNEKVGDVVLPWASSPEDFIQQHRALESEYVSAHLHEW
 IDLIFGYKQRGPAEEALNVFYCYEGAVDLDHVTDERERKALEGIISNFGQTPCQLLKEP
 HPTRLSAEEAAHRLARLDTNPSPIFQHLDELKAFFAEVTVSASGLLGTHSWLPYDRNISNYF
 SFSKDPMTGSHKTQRLLSGPWPVPGSGVSGQALAVAPDGKLLFSGGHWGDSLRVTALPRGKLL
 SQLSCHLDVVTCLALDTCGIYILISGRDTCMVWRLLHQGGLSVGLAPKPVQVLYGHGAAS
 CVAISTELDMAVSGSEDGTVIHTVRRGQFVAALRPLGATFPGPIFHLALGSEGQIVVQSSA
 WERPGAQVITYSLHLYSVNGKLRLASLPLAEQPTALTVTEDFVLLGTAQCALHILQLNTLLPAA
 PPLPMKVAIRSVAVTKERSHVLVGLEDKLIVVAGQPSEVRSSQFARKLWRSSRRISQVSS
 GETEYNPTAR

N-glycosylation site.

amino acids 677-681

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 985-989

Tyrosine kinase phosphorylation site.

amino acids 56-65, 367-376, 543-551

N-myristoylation site.

amino acids 61-67, 436-442, 604-610, 610-616, 664-670, 691-697,
 706-712, 711-717, 769-775, 785-791, 802-808, 820-826, 834-840,
 873-879, 912-918, 954-960

FIGURE 24

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCC
 CACGGCCCACTTTGTGAACCTCTCGTGCCAGGGCTGATGTGCGTCTTCCAGGGCTACTCAT
 CCAAAGGCCATAATCCAACGTTCTGTCTTCAATCTGCAAAATCTATGGGGTCTGGGGCTCTTC
 TGGACCCTTAACTGGGTACTGGCCCTGGGCCAATGCGTCCTCGTGGAGCCTTTGCCTCCTT
 CTACTGGGCCTTCCACAAGCCCCAGGACATCCCTACCTTCCCTTAAATCTCTGCCTTCATCC
 GCACACTCCGTTACCACACTGGGTCATTGGCATTGGAGCCCTCATCCTGACCCTTGTGCAG
 ATAGCCCGGGTCATCTTGGAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCTGTAGC
 CCGCTGCATCATGTGCTGTTTCAAGTGTGCCTCTGGTGTCTGGAAAAATTTATCAAGTTC
 TAAACCGCAATGCATACATCATGATCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAA
 AATGCGTTCATGCTACTCATGCGAAACATTGTGAGGGTGGTGTCTGAGCAAAAGTCACAGA
 CCTGCTGCTGTCTTTGGGAAGCTGCTGGTGGTCGGAGGCGTGGGGGTCTGTCTCTCTTTT
 TTTTCTCCGGTCGCATCCCGGGGCTGGGTAAAGACTTTAAGAGCCCCACCTCAACTATTAC
 TGGTGCCCATCATGACCTCCATCCTGGGGGCTATGTCATCGCCAGCGGCTTCTTACGCGT
 TTTCGGCATGTGTGTGGACACGCTCTTCTCTGCTTCTTGGAGACCTGGAGCGGAACAACG
 GCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAAAGATTCTGGGCAAGAAGAAC
 GAGGCGCCCCCGGACAACAAGAAGAGGAAGAAGTGAAGCAGCTCCGCGCCTGATCCAGGACTGC
 ACCCACCCACCGTCCAGCCATCCAACCTCACTTCGCCTTACAGGTCTCCATTTTGTGGT
 AAAAAAAGGTTTTAGGCCAGGCGCGTGGCTCACGCCGTGAATCCAACACTTTGAGAGGCTG
 AGGCGGGCGGATCACTGAGTCAGGAGTTTCGAGACCAGCCTGGCCAACATGGTGAAACCTCC
 GTCTCTATTAATAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCTATCCAGCTAC
 TCGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTGCACTGAGCCGAGA
 TCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAA
 AAAGATTTTATTAAGATATTTTGTAACTC

FIGURE 25

RTRGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVLG
LFWTLNWWLALGQCVLAGAFASYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFGALILTLVQ
IARVILEYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAK
NAFMLLMRNIVRVVLDKVTDLLFFGKLLVVGGVGLSFFFFSGRIPGLGKDFKSPHLNYY
WLPIMTSILGAYVIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYMSKSLKILGKKK
EAPPDNKKRKK

FIGURE 26

GAGTCTTGACCGCCGCCGGGCTCTTGGTACCTCAGCGGAGCGCCAGGCGTCCGGCCGCCGT
 GGCT**ATG**TTTCGTGTCCGATTTCGCCAAAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCC
 TTCTCTTCGTGGCCTCGGACGTGGATGCTCTGTGTGCGTGCAAGATCCCTCAGGCGCTTGTTTC
 CAGTGTGACCACGTGCAATATACGCTGGTTCAGTTCCTGGGTGGCAAGAAGCTTGAAAGTGC
 ATTTCTTGAGCATAAAGAACAGTTTCATTATTTTATCTCATAAAGTGTGGAGCTAATGTAG
 ACCTATTGGATATTCTTCAACCTGATGAAGACACTATATTCTTTGTGTGACTCCCATAGG
 CCAGTCAATGTCGTCATGTATACAACGATACCCAGATCAAATTACTCATTAAACAAGATGA
 TGACCTTGAAGTTCGCCCTATGAAGACATCTTCAGGGATGAAGAGGAGGATGAAGAGCATT
 CAGGAAATGACAGTGTGGGTGACAGCCTTCTGAGAAGCGCACACGGTTAGAAGAGGAGATA
 GTGGAGCAAACCATGCGGAGGAGGCAGCGCGAGAGTGGGAGGCCCGAGAAGAGACATCCT
 CTTTGACTACGAGCAGTATGAATATCATGGGACATCGTCAGCCATGGTGTGTTGAGCTGG
 CTGGATGCTGTCCAAGACCTGAATGACATGCTGTGGTGGGCCATCGTTGGACTAACAGAC
 CAGTGGGTGCAAGACAAGATCACTCAAATGAAATACGTGACTGATGTTGGTGTCTGCAGCG
 CCACGTTTCGCCCAACAACACCGGAACGAGGATGAGGAGAAACACTCTCCGTGGACTGCA
 CACGGATCTCCTTTGAGTATGACCTCCGCCTGGTGCTCTACCAGCACTGGTCCCTCCATGAC
 AGCCTGTGCAACACCAGCTATACCGCAGCCAGGTTCAAGCTGTGGTCTGTGCATGGACAGAA
 GCGGCTCCAGGAGTTCCTTGACAGACATGGGTCTTCCCTGAAGCAGGTGAAGCAGAAGTTCC
 AGGCCATGGACATCTCCTTGAGGAGAATTTGCGGGAATGATTGAAGAGTCTGCAAAATAAA
 TTTGGGATGAAGGACATGCGCGTGCAGACTTTCAGCATTCATTTTGGGTTCAAGCACAAGTT
 TCTGGCCAGCGACGTGGTCTTTGCCACCATGTCTTTGATGGAGAGCCCCGAGAAGGATGGCT
 CAGGGACAGATCACTTCATCCAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTG
 TACCATGGCCTGGAAGTGCACAAGAAGCAGCTGCGAGCCACCCAGCAGACCATTCAGCTGC
 CTTTGACCAACCTCGTCATCTCCAGGGCCTTTCTGTACTGCTCTCTCATGGAGGGCAC
 TCCAGATGTGATGCTGTTCTCTAGGCCGGCATCCCTAAGCCTGCTCAGCAAACACCTGCTCA
 AGTCCTTTGTGTGTTGACAAAGAACCAGCGCTGCAAACTGCTGCCCTGGTGTGCTGCC
 CCCCTGAGCATGGAGCATGGCACAGTGACCGTGGTGGGCATCCCCCAGAGACCGACAGCTC
 GGACAGGAAGAACTTTTTGGGAGGGCGTTTGAGAAGGCAGCGGAAGACACAGCTCCCGGA
 TGCTGCAACAACCATTTTGACCTCTCAGTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTT
 CTGGACGCATTATTTCCCTCCTGTCT**TAG**GAATTTGATTCTCCAGAATGACCTTCTTATT
 TATGTAAGTGGCTTTCATTTAGATTGTAAGTTATGGACATGATTTGAGATGTAGAAGCATT
 TTTTATTAATAAATGCTTATTTTAGGAAA

FIGURE 27

MFVSDFRKEFYEVVQSQRVLLFVASDVDALCACKILQALFQCDHVQYTLVPVSGWQELETAF
LEHKEQFHYFILINCGANVDLLDILQPEDDTIFFVCDSHRPVNVVNVYNDTQIKLLIKQDDD
LEVPAYEDIFRDEEEDDEHSGNDSGSEPSEKRTREEEIVEQTMRRRQRREWEARRRDILF
DYEQYEHGTSSAMVMFELAWMLSKDLNDMLWVAIVGLTDQWVQDKITQMKYVTDVGVLQRH
VSRHNHRNEDEENTLSVDCTRISFEYDLRLVLYQHWSLHDSLNCNTSYTAARFKLWSVHGQKR
LQEFLLADMGLPLKQVKQKFQAMDISLKENLREMIIESANKFGMKDMRVQTFSIHFGFKHKFL
ASDVVFATMSLMESPEKDGSGTDHFIQALDSLRSNLDKLYHGLELAKKQLRATQQTIASCL
CTNLVISQGPFLYCSLMEGTPDVMLFSRPASLSLLSKHLLKSFVCSTKNRRCKLLPLVMAAP
LSMEHGTVTVVGI PPETDSSDRKNFFGRAFEKAAESTSSRMLHNHFDLSVIELKAEDRSKFL
DALISLLS

FIGURE 28

GTACCTCAGCGCGAGCGCCAGGCGTCCGGCCGCCGTGGCTATGNTCGTGTCCGATTTCCGCA
AAGAGTTTCTACGAGGTGGTCCAGAGCCAGAGGGTCCTTCTCTTCGTGGCCTCGGANGTGGAT
GCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTCCAGTGTGACCANGTGCAATATANGCT
GGTTCAGTTTCTGGGTGGCAAGAACTTGAACTGCATTTCTTGAGCATAAAGAACAGTTTC
ATTATTTTATTCTCATAAACTGTGGAGCTAATGTAGACCTATTGGATATTCTTCAACCTGAT
GAAGACACTATATTCTTTGTGTGTGACCCCATAGGCCAGTCAATGTTGTCAATGTATACAA
CGATACCC

FIGURE 29

CAGGAACCCCTCTCTTTGGGTCTGGATTGGGACCCCTTTCAGTACCAATTTTTCTAGTGAAC
 CACGAAGGGACGATACCAGAAAACACCCCTCAACCCAAAGGAAATAGACTACAGCCCCAATTG
 GCTGACTTTGGCTATAGAAAAAAGAAAGGAACGAAAAGACAGTTTTTTTTGGAAAGCTAA
 GTCTTCCCTTTATCGAGTCAAGAAAACCCCCCTTCTTGAGCTATTTACAGCTTTTAAACAATT
 GAGTAAAGTACGCTCCGGTCACCATGGTGACAGCCGCCCTGGGTCCCGTCTGGGCAGCGCTC
 CTGCTCTTTCTCCGTGATGTGTGAGATCCGTATGGTGGAGCTCACTTTTGACAGAGCTGTGGC
 CAGCGCTGCCAACCGGTCTGTGACTCTGAGGACCCCTGGATCTGCCCATGTATCTCAG
 CCTCTTCTCCGGCCGCCCCACGCCCTGCTGAGATCAGACCCCTACATTAATATACCATC
 CTGAAGGGTGACAAAGGGGACCCAGGCCAATGGGCCCTGCCAGGTACATGGGCAGGGAGGG
 TCCCCAAGGGGAGCTGGCCCTCAGGGCAGCAAGGGTGACAAAGGGGAGATGGGCAGCCCCG
 GCGCCCCCTGCCAGAAGCGCTTCTTCGCCCTTCTCAGTGGGCCGCAAGACGGCCCTGCACAGC
 GGCGAGGACTTCCAGACGCTGCTCTTCGAAAGGGTCTTTGTGAACCTTGATGGGTGCTTTGA
 CATGGCGACCCGCGAGTTTGTGCTGCTCCCTGCTGGCATCTACTTCTTACGCTCAATGTGC
 ACAGCTGGAATTACAAGGAGACGTACGTGCACATATGCATAACAGAAAGAGGCTGTATC
 CTGTACGCCGACGCCAGCGAGCGCAGCATCATGCAGAGCCAGAGTGTGATGCTGGACCTGGC
 CTACGGGGACCCGCTCTGGGTGCGGCTCTTCAAGCGCCAGCGCGAGAAGCCATCTACAGCA
 ACGACTTCGACACCTACATCACTTTCAGCGGCCACCTCATCAAGGCCGAGGACGACTGAGGG
 CCTCTGGGCCACCTCCCGGCTGGAGAGCTCAGGTGCTGGTCCCTCCCTTCAGGGCTCAG
 TTGCACTGCTGTGAAGAGCAAGGCCAGGGAGGTCCCGGGGACTGGCATTCTGGGGAGA
 CCTGCTTCTATCTTGGCTGCCATCATCCCTCCAGGCTATTTCTGCTCCTCTCTTCTCTCT
 TGGACCTATTTTAAAGACTTGTCAACCTAAATATTCTAGAAGCTTCCAGCCTCGTAGGCC
 AGCAGTCTCTCAAACCTTGAAATGTCATGCCAATCACCAGGGGTCTCGTGTAAATGCAAGTCT
 GACTCAAGAGCTGAGTGGGTCCAGGATTCTGTGTTTCTCATATGTCTCTGGGTGATGCTG
 ATGGGGTCAGTCTATTGAACCACTGGAGCAACCCAGGTCTTAGGACTTTCTCAATATTCTAG
 TACTTTCTGAACATTCTGGAATCTCCACATTTCTAGAATTTCTCCAACATTTTTTTTCT
 TGAGACAGTCTTGTCTGTGTGCCAGGCTAGAGTGCAGTGGTGCAATCTCAGTTCACTGC
 AACCTCTGCTCCCGGGTCAAGCGATTCTTCTGCTCAGCCTCCCTAGTGGCTGGGATTAC
 AGGCGCTGCTACCATGCTGGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTACCATA
 TTGGCCAGGCTGGTGTGAACCTCTGACTTCAGGTGACCCACCCGCTCGGCCCTCAAAAAT
 GCTGGGATTCAGAGTGTGAGCCACCGTGCTGGCCAATTCCAACATTTCTAAATTTCTCTAT
 CCTCCAGGCTCCCGGTGCTATGTTCTCTTTACCCCTTCCCTCTTCTCTTGTCTCAGGCC
 TGCAACCTGACGCCACCGTTCAATTTATTCAATTAACACTGAGCACTCACTCTGTGCT
 GGGTCCCGGGAAGGGTGAGGGGGTCAGACACAGGCCCTGCCCTCAGTGAAGTGGCCCA
 GTCCAGCCAGCGGGGAGAGATGTGTACATAGGTTTTAAAGCAGCCAGAGCTCATGGGG
 GCTGTGTTCTGGGTGTTCAAGTGCTGCTGGTCTCCATTACCCACTGCTCCCAAGCTGG
 TGGGACGGGTCCCGGTGGCAGGGGAGGTATCTCCTTCCCGTCTCTATCCACCTGCCCGAG
 TGCTCATCGTTACAGCAACCCAGGGGCTTGGCCAGGTCAAGGGTTCTGTGAGGAGAGG
 ACCCAGGAGTGTGGGGGCAATTTGGGGGGTGAAGTGGCCCCGGAAGATGGAACCCACACCA
 TAGCTCTCCCAACAGCTGATACGGCATCTGCGAGAAGACCTGCTCCTCACTGGGATCCC
 CTTCCTGCTCTCTCCAGGGCTCTGCCAGGGCTTGCTCAGTCCCTTCCACCAAAGTCACT
 GAACTTCCGTTTCCCAAGGGCTCTCAGCTGCCCTCAGACACTGATGTCTGTCCCCAGGTGCT
 CTCTGCCCTCATGCCCTCTCACCAGCCAGTCCCGGACTCTCCAGGCTTTATCAAGGTG
 CTAAGGCCCGGGTGGCGAGCTCCTCGTCTCAGAGCCCTCCCGGCTGGTGTCTGCTTTAC
 AAACACCTGACAGGAGAAGGGGCCAGGAAGCCCCAGGCTTTAGAGCCCTCAGCAGGTCTGGG
 AGCTAGAGCAAAAGGAGGACCTCAGGCGTTCCGTTTCTTCTTCCAGGGTGGGGTGGCCCTGGT
 GTTCCCCTAGCTCTCCAACCCAGGTGGCCTGCCCTTCTCCCAAGGGAGGGCCGCTCCGC
 CCATTGGTGTCTCATCGGACTCTGGGCTGAGGTGCCCGGGGGTGTACTCTGGTGTCTCAC
 AGCCGAGGGAGCCGTGGCTTCATGGCCAGATGACGGAACAGGGGTCTGACCAAGTGGCAGGA
 AGACCTGTGCTATAAACACCCCTGCTGATCTGCCCTGCCCTGACCCGCCACGCCCTGCC
 GTCCAGCATGATTAAGAATGCTGCTCCTCTTGGAAAAA

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ACTCGAACGCGAGTTGCTTCGGGACCACGAGACCCCTCGGGCCGACCCGCCAGGAAGACTG
 AGGCCGCGGCCTGCCCGCCGCGCTTCCTTGCGCCGCGCCGCTCCCGGGACAGAAAG**ATG**TG
 CTCACAGGTCFCCCTCTGCTGCTGCCGCTGCTCTCTGCTACTGGCCCTGGGGCTGGGGTCAGG
 GCTGCCCATTCGCGCTGCCAGTGCAGCGACGCCACAGACAGCTCTTCTGCATTGGCCGCCACGGG
 ACCACGGTGCCCGCAGAGCTGCCACCCGACACGGTGGGGCTGTACGTTCTTTGAGAAGCGCAT
 CACATGCTCGACGACGAGCAGCTTTTGGCGGCTTGC GGCGCTGCAGCTCTTGGACCTGTAC
 AGAAACAGATCGCCAGCTGCCACGGGGGTCTTCACAGCACTGCCCAACCTCAGCAACCTG
 GACCTCAGCGCCAAAGCTGCATGAATCAACAACTAGACACTTCGTGGCTCGGGCGCC
 CGAGCGCCTTACCTGGGCAAGAACCGCATCCGCCACATCCAGCCTGGTGCTTCGACACG
 TCGACGCTCTCGGAGCTCAAGCTGCAGGACAACAGCTCGGGGCACTGGCCCGCTGGCTCGGCT
 CTGCCCGGCTGCTGCTGTGCTGACTCAGGCCAACAGCCTCTGGCCCTGGAGCCCGCAT
 CCTGTGACACTGCCAACAGTGGAGCGCTGCGGCTGGCTGGTCTGGGCTCGACAGCACTGGACG
 AGGGGCTCTTACGCGCTTGCAGCACTCCAGCACTGGATGTGTCCACAAACAGCTGGAG
 CGAGTGCCACTGTATCCGAGGCTCTCGGGGCTGACGCGCTGCGGCTGGCCGGCAACAC
 CGCATATGCCAGCTCGGCCCGAGGACACTGGCCGAGCTTGGCTGCCCTCGAGGAGCTGGATG
 TCGCAACCACTAAGCTCGAGGCGCTGCTGGCAGCTCTTGGGCTCTTCCCGGCTCGCG
 CTGCTGGCAGCTGCCGCAACCCCTTCAACTGCGTGTGCCCTCTGAGCTGGTTTGGCCCGCTG
 GGTGCGGAGAGCGACGTGCATCACTGGCCAGCCTGAGGAGACGCGCTGCCACTTCCGCCCA
 AAGCTCTGGCCGCGTCTCTTGGAGCTTGACTACCGCACTTTGGCTGCCAGGCCACACC
 ACCACAGCCAGCACTGCCAACCCAGCGCCGCTGGTGGCGGAGCCCAAGCACTTGCTTTAG
 CTGTGGCTCCTACTGGCTTAGCCCCAGGCCGCCGCACTGAGGCCCCAGCCGCCCTCA
 CTGCCCAACGACTGTAGGGCTGTCCCCAGCCCCAGGACTGCCACCCTCCACCTGAGCTT
 AATGGGGGCACTGCCACTGGGCAACGCCACCACTGGCGTGTGTGCCCTACGGGCTT
 CACGGGCTGTACTGTAGAGCCAGATGGGGCAGGGGACAGCCGCAACCCCTACACAGTCA
 CGCCGAGGCCACACAGTCTCTTGACCTGGGCACTGAGCCGGTGTAGGCCCACTCTCTCGCG
 GTGGGGCTGCAGCGCTACCTCAGGGGAGCTCCGTGCAGCTCAGGAGCTCCGTTCACTCA
 TCGCAACCTATCGGGCCTGATAAGCGGCTGGTAGCTGCGACTGCGCTGCTCGCTGCTG
 AGTACAGCGTACACCAAGCTCGGCCGCCACGCCCACTTACTCGGTCTGTGTCATGCTTTGGG
 CCGGGCGGCTGCCCGAGGGCGAGGAGCTGCGGGAGGGCCATACACCCAGCGCTCCA
 CTCCAACCAGCCCCAGTACCCAGGCGCGCGAGGCAACCTGCCGCTCTTCACTTGCGCCG
 CCTTGGCCCGGCTGCTCTGGCCGCTGGCTGCGGTGGGGGCACTGCTGTGCGCGG
 GCGGGGCACTGGACAGCGGCTCAGGACAAGGGCAGGTGGGGCAGGGGCTGGGCCCT
 GGAATCGAGGGAGTAGAGGTCOCCTTTGGAGCCAGGCCGGAAGGCAACAGAGGCGGTGGAG
 AGGCCCTGCCAGCGGCTGAGTGTGAGGTGCCACTATGGGCTCCAGGGGCTGGGCTCA
 CAGTACACCCCTCCACGCAAGGCCCTAGCT**CTA**AGCCAGAGAGACAGGGCAGCTGGGGCG
 GGCTCTCAGCGAGTGAAGTGGCCAGCCCCCTCTGCTGCCACACAGCTAAGTCTTCAGTCC
 CAACCTCGGGGATGTGTGACAGAGGCTGTGTGACCAAGCTGGGCGCTTTCCTCTGGA
 CCTCGTCTCTCTACTCTGTGAGATGCTGTGGCCAGCTGACGAGCCTTAAGCTCCCGAACG
 CGAGTGCCCTATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGAGTCTCCCTGGGACGGG
 GCGCCTGCCATGTGCTGTGAACGATGCTTGGGTCTGTGGCTCTCCCACTCCAGGCGGA
 CCTTGGGGGCGAGTGAAGGAAGCTCCCGGAAGAAGCAGAGGGAGAGCGGGTAGGCGGTGTG
 TGACTCTAGTCTTGGCCCGAGGAGCGAAGGAAGCAAAAGAACTGGAAGGAAGATGCTTAA
 GGAACATGTTTTGCTTTTTTAAATATATATATTTATAAGAGATCCTTCCCATTTATTCTG
 GGAAGATGTTTTTCAAATCAGAGCAAGGACTTTGGTTTTTGAAGACAACAGATGATAT
 AAGGCTTTTTGTAAAGAAAAATAAAGATGAAGTGTGAAA

MCSRVP LLLPL LLL L L L A L G P G V Q G C P S G C Q C S Q P Q T V F C T A R Q G T T V P R D V P D T V G L Y V F E N
G I T M L D A G S F A G L P G L Q L L D S Q N Q I A S L P S G V F Q P L A N S N L D L T A N R L H E I T N E T F R G L R
R L E R L Y L G K N R I R H I Q P A G F D T L D R L E L K L Q D N E L R A L P P L R L P R L L L D L S H N S L L A L E P
G I L D T A N V E A L R L A G L G L Q L D E G L F S R L R N L H D L D V S D N Q L E R V P P V I R G L R G L T R L R L A G
N T R I A Q L R P E D L A G L A A L Q E L D V S N L S L Q A L P G D L S G L F P R L R L L A A A R N P F N C V C P L S W F G
P W V R E S H V T L A S P E E T R C H F P P K N A G R L L L E D Y A D F G C P A T T T T A T V P T T R P V V R E P T A L S
S S L A P T W L S P T A P A T E A P S P P S T A P T V G P V P Q P Q D C P P S T C L N G G T C H L G T R H H L A C L C P E
G F T G L Y C E S Q M G Q T R P S P T P V T P R P P R S L T L G I E P V S T P L R V G L Q R Y L Q G S S V L R G L S R L R
T Y R N L S G P D K R L V T L R L P A S L A E Y T V T Q L R F N A T Y S V C M L G R G R V P E G A E C A G E A H T P P A
V H N S H A P Q T Q A R E G N L P L L I A A A V L L A A A V G A A Y C V R R G R A M A A A Q D K G Q V G P G A G
P L E L E G V K V P L E P G P K A T E G G E A L P S G S E C E V P L M G F G P G L Q S P L H A K P Y I

FIGURE 33

GAATCATCCACGCACCTGCAGCTCTGCTGAGAGAGTGAAGCCGTGGGGGTTTTGAGCTCAT
 CTTTCATTCATATGAGGAATAAGTGGTAAAACTCTGGAAAAACATGAGACTCATCAG
 AAACATTTTACATATTTGTAGTATTGTTATGACAGCAGAGGGTGATGCTCCAGAGCTGCCAG
 AAGAAGGGAACATGATGACCAACTGCTCCAACATGTCTCTAAGAAAGGTTCCCGCAGACTTG
 ACCCAGGCCACAACGACACTGGATTTTCTATAACCTCCTTTTCAACTCCAGATTTTCTAGA
 TTTTCTATCTGTCTCCAACCTGAGAGTTTTGATTCTATGCCATAACAGAAATTCACACAGCTGG
 ATCTCAAAACCTTTGAATTTCAACAAGGAGTTAAGATATTTAGATTTGTCTAATAACAGACTG
 AAGAGTGTAACTTTGGTATTTACTGGCAGGTCTCAGGTATTTAGATCTTTCTTTTAATGACTT
 TGACACCATGCCCTATCTGTGAGGAAGCTGGCAACATGTCAACCTGGAAGATCCTAGGTTTGA
 GTGGGGCAAAAAACAAAAATCAGATTTCCAGAAAAATGCTCATCTGCATCTAAATACTGTC
 TTCTTAGGATTCAGAACTCTTCCCTATTATGAAGAAGGTAGCCTGCCCATCTTAAACACAA
 AAAACTGACATTTGTTTTACCAATGGACACAAATTTCTGGGTCTTTTTCGCTGATGGAATCA
 AGACTTCAAAAAATATTAGAAATGACAAATATAGATGGCAAAAGCCAAATTTGTAAAGTTATGAA
 ATGCAACGAAATCTTAGTTTGAAGAAATGCTAAGACATCGGTTCTATTGCTTAATAAAGTTGA
 TTTACTCTGGGACGACCTTTTCCCTTATCTTACAATTTGTTTGGCATAACATCAGTGGAACT
 TTCAGATCCGAAATGTGACTTTTGGTGGTAAGGCTTATCTTGACCACAAATTCATTTGACTAC
 TCAAATACTGTATGAGAACTATAAAATTTGGAGCATGTACATTTAGAGTGTTTTACATTCA
 ACAGGATAAAATCTATTGCTTTTGACCAAAATGGACATGAAAAACCTGACAATATCAAATG
 CCAAAATGCCACACATGCTTTTCCGGAATTTCTCTAGAAAATTTCAATTTTAAATTTTGGC
 AATAATATCTTTACAGACGAGTTGTTTAAAGAACTATCCAATGCCCTCACTTTGAAAACCTCT
 CTTTGTGAATGGCAATAAATCGGAGACACTTTCTTTAGTAAGTTGCTTTGTCTAAACACAGAC
 CCTTGGAACTGTTGATCTGAGTCAAATCTATTACACATAAAAAATGATGAAATTTGCTCA
 TGCCCAAGAACTGGGTCAAATGAACTGTCTGATCAATAAATTTGCTGATCTGCTCTCAG
 GTGCTTGCCCAAAAGTATTCAAATACTTGACCTAAATTAATAACCAAAATCCAACTGTACCTA
 AAGAGACTATTCATCTGATGGCCTTACGAGAACAATAATTTGCACTTTAATTTTCTAATGAT
 CTCCCTGGATGTCAGTCAATTTAGTAGACTTTCAGTTCTGAACATTTGAAATGAACTTCATTCT
 CAGCCCATCTCTGGATTTTGTTCAGAGCTGCCAGGAAGTTAAACCTCTAAATGCCGGAAGAA
 ATCCATTTCCGGTGTAACCTGTGAATTAATAAATTTCAATTCAGCTTGAAACATATTTAGAGGTC
 ATGATGGTTGGATGGTCAGATTTCATACACCTGTGAATACCTTTAAACCTAAGGGGAACTAG
 GTTAAAGAGCTTTCATCTCCACGAATTTATCTGCAACACAGCTCTGTTGATTGTCCACCATTT
 TGGTTATTATGATGTTCTGGGGTTGGCTGTGGCCTTCTGCTGTCTCCACTTTGATCTGCC
 TGGTATCTCAGGATGCTAGGTCAATGCACACAACATGGCACAGGTTAGGAAAAACAACCCA
 AGAACAACTCAAGAGAAATGTCCGATTTCCACGCATTTATTTTCATACAGTGAACATGATCTCT
 TGTGGGTGAAGAATGAATTTGATCCCCAATCTAGAGAAGGAAGATGGTTCTATCTTGATTTGC
 CTTTATGAAAGCTACTTTTGACCTGGCAAAAGCATTAGTGAAATATTGTAAAGCTTCATTGA
 GAAAAGCTATAAGTCCATCTTTGTTTGTCTCCCACTTTGTCCAGAATGAGTGGTGCCATT
 ATGAATCTACTTTTGGCCACCACAATCTCTTCCATGAAAATTTCTGATCATATAATTTCTATCT
 TTACTGGAACCCATTCCTATTTGATTTCCCACTCCACAGGTATCATAAACTGAAAGCTCTCTCT
 GGAAAAAAGCATACTTTGGAATGGCCAAAGGATAGCGTAAATGTGGGCTTTTCTGGGCA
 ACCCTCGAGCTGCTATTAATGTAAATGTATTAGCCACAGAGAAATGTATGAATCGCAGACA
 TTTACAGAGTTAAATGAAGAGCTCTCGAGGTTCTACAATCTCTCTGATGAGAACAGATTTGTCT
 ATAAATCCCACTGCTTTGGGAAGTTGGGGACCACATACACTGTTGGGATTTACCTTTGATTA
 CAACCTTTATGTCGAATTTGCAAAATTTTATAAATAAAAAATGGTTATTCCTTCATA
 TCAGTTTCTAGAAGGATTTCTAAGAAATGATCTCTATAGAAACACCTTCACAAGTTTCTATAAGG
 GCTTATTTGAAAAGAGTGTTCTATCCAGGATTTGTTTATAATCATGAAAATGTGGCCAGGTGCG
 AGTGGCTCACCTTTGTAATCCAGCACTATGGGAGGCCAAGTGGGTGAGCCACAGGAGGTCAA
 GAGATGAGGACCTCTCTGGCCCAACATGGTGAACCCCTGTCTCTATAAAAAACAAAAATTA
 CTGGGGCGTGATGGTGCAGCCCTGTAGTCCAGCTACTTTGGGAGGCTGAGCGAGGAGGAATCG
 CTTGAACCCCGGAGGTGCGAGTTGCGATGAGCTGAGATCGAGCCATGCACTCCAGCTGGT
 GACAGAGCGGAGACTCCATCTCAAAAAAAGAAAAAAGAAAAAATGGAACATCC
 TCATGGCCACAATAAAGTCTAATTCATAAATATATAGTACATTAATGTAAATATATATTA
 CATGCCACTAAAAAGAAATAGGTAGCTGTATTTTCTGGTATGAAAAACATATTAATAT
 GTTATAAATATAGGTTGGTGCAAACTAATTTGTTGGTTTGGCATGAAATGGCATTTGAA
 ATAAAAAGTGTAAAGAAATCTATACCAGATGTAGTAACAGTGGTTGGGCTCTGGGAGTTGGA
 TTACAGGAGACTTTGATTTCTATGTTGTATTTCTATAATGTTTGAATTTGTAGATGA
 ATCTGTATTTCTTTTATAAGTAGAAAAAATAAAGATAGTTTTCACAGCCT

CGCGGAAATTTTATTTT

FIGURE 34

MRLIRNIYIFCSI VMTAEGDAPELPEERELMTNCSNM SLRKVPADLT PATTTLDLSYNLLFQ
LQSSDFHSVSKLRVLILCHNRIQQLDLKTFFFNKELRYLDLSNNRLKSVTWYLLAGLRYLDL
SFNDFDTMPICEEAGNM SHLEILGLSGAKIQKSD FQKIAHLHLNTVFLGFRTLPHYEEGSLP
ILNTTKLHIVLPMDTNFWVLLRDGIKTSKILEMTNIDGKSQFVS YEMQRNLSLENAKTSVLL
LNKVDDLWDDLFLILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFR
VFYIQQDKIYLLLT KMDIENLTISNAQMPHMLF PNYPTKFQYLN FANNILTDELFKRTIQLP
HLKTLILNGNKLETL SLVSCFANNTPLEHLDLSQNL LQHKNDENCSWPETVVNMNLSYNKLS
DSVFRCLPKSIQILD LNNNQIQTVPKETIHLMALREL NIAFNFLTDLP GC SHFSRLSVLNIE
MNFILSPSLDFVQSCQEVKTLNAGRNPFRCTCELKNFIQLE TYSEVMVGVWSDSYTCEYPLN
LRGTRLKDVLHLS CNTALLIVTIVVIMLVGLAVAF CCLHFDLPWYLRMLGQCTQTWHRV
RKTTQEQLKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSI SENI
VSFIEKSYKSIFVLPSPNFVQNEWCHYEFYFAHNL FHENSDHIILILLEPIPFYCIPTRYHK
LKALLEKKAYLEWPKDRRCGLFWANLRAAINVNVLATREMYELQTFTELNEESRGSTISLM
RTDCL

FIGURE 35

GGGGGCTTTCTTGGGCTTGGCTGCTTGGAAACCTGCCTCCAAGGACCGGCTCGGAGGGGTGCGCGGAAAGG
 GAGGGAAAGGAAGGGCGGGGCGGGCCCCCTGCGCGCGCGCGCGCTCTGCGCGCGCCCTGTCGCGCGCGG
 CCAGCCAGCGCCAGCCCGGGGGCGGTACACAGCGCAGCCAGCGCGCGCTCCCGCGCCAAAGCGCGCGCT
 CTGCTGTGGCTTGGCGCTTGGCCCGCGCCAGCTTCTGCGCGCGCAGCCCGCGCGCGCGCGCGCTGACCGTGA
 CCTGCGCTCGGCGGGGCGGAGCAGGCAATGCTCCCGCGCGGGGACCGTACCCAGCGCTGGCCCTGGTGCTC
 CTGGCAGTGACCTGGCGGGGTGAGAGCCAGGGCGCAGCCCTCGAGGACCCCTGATTATAGCGCGAGGAGAT
 CATCGAGGGAGACTCAACATCCAGGCGGGCATTAATGAAATGATTTTTATGACGAGAGCTGGTGCGCGGGAAG
 CCGGGAGAGATGGAGCGCGCGCGCAGGAGCCAGCGCGCCCAAGAGGGCCACCAAGCCCAAGAAAGCTCC
 AAGAGGGAGAGATCGGCTCGGAGCGCGCTCCACAGGTAAACACAGCAACAAAAGATTATGAGAACCAAGAG
 CTCTGAGAAGGCTGCCAACGATGATCAGAGTGTCCGTGTGGCCCGTGAAGATGTCAAGAGAGATTGCCACCTC
 TTGGTCTGGAAACCTTAAAAATCAGAGACTTCCAGCTCCATGCTCCACGCTGAAGCGCTTATGGCTGGGGCA
 CATCGAGGGAGACTCAACATCCAGGCGGGCATTAATGAAATGATTTTTATGACGAGAGCTGGTGCGCGGGAAG
 AAATGACCTCCAGCAGTGGATGAAAGTGGATGCTGGCGCTGACCAAGATTCACTGGTGTCACTCAAGGA
 GGAACCTCCTCTGGCTGAGTGCTGGGTGACATCCTAATAGGTCACTGGTGAGCAATGACACCCACACGTTGGGT
 ACTGTTAAGAAATGGATCTGAGAGATGATATTTGAGGGAAACAGTGAGAAGGAGATCCCTGTTCTCAATGAGCT
 ACCCGTCCCCATGGTGGCCGCTACATCCGCTAAACCTCACTGCTGGTTTGATAATGGGAGCATCTGCATGA
 GAATGAGATCTCTGGCTGCCACTGCCAGATCTAATAATTTATACCGCGCGGAACGAGATGACCCACACT
 GAGGCTGGATTTAAGCACCAATATAAGGAATGCGCAGTTGATGAAAGTTGTGAATGAAATGTGCTGTC
 CAATATCACCAGAAATTAACACATTTGAAAAGCCACAGGGCCTGAAGCTGTATGCTGTGGAGATCTCAGATC
 ACCCTGGGAGCATGAAGTCGGTGAGGCCGAGTTCCACTACATCGCGGGGGCGCCAGCGCAATGAGTGCTGGCG
 CGGAGATGCTGCTGCTGTGGTGAGTTCGTGTGTGAGGAGTACTTGGCCCGGAATGCGCGCATCTGTCACCT
 GGTGGAGGACCGGGATTACGTCCTCCCTCCCTCCCTCAACCCGATGGTGAGAGGCTACGAAAGGGGT
 CGGAGCTGGGAGGCTGGTCCCTGGGAGCGTGGACCCACGATGGAATTGACATCAACCAACTTTCTTGATTTA
 AACACGCTGCTCTGGGAGCGAGGATCGACAGAATGTCCCGAGGAAGTTCCCATCACTATGATGCAATCCC
 TGAGTGGTTTCTGTGGAAATGCCACGCTGGCTGCCAGAGACGAGAGCATATAGCTGGATGGAATAAATCC
 CTTTTGTGCTGGGCGCAACTCGAGGGCGCGAGCTGGTGCTGGCTATCCCTACGACCTGGTGCGTCCCC
 TGGAGAGCGAGGAACACACCCGCCACCCCGATGACCAAGTGTTCGCTGGCTGGCTACTCTATGCTCCAC
 ACACCGCTCATGACACAGCGCGGAGGAGGTGTGCCACAGGAGCACTCCAGAAGGAGGAGGCACTGCA
 ATTGGGCTCCTGGCACACGCTCGCTGGAAGTCTGAACGATTTCACTACCTTCATACAACTGCTTCGAAGT
 TCCATCTACGCTGGCTGTGATAAATACCCACATGAGAGCGAGCTGCCCGAGGATGGGAGAATAACCGGGAATC
 TCTGATCGTGTTCATGAGAGAGGTTTCACTGGCATTAAGAGCTTGGTGAGAGATTACATGGAAGGAATCC
 CAAACGCCATTATCTCCGTAGAAGCATTAACCATGACATCGAACAGCCACGATGGGAGATTACTGGCGCTC
 CTGAACCTGGAGATATGTGGTCAGACAAAGGCGGAAGGTTTCACTGATCCACCAAGATCTGTATGGTGTG
 CATATGACCTGGGAGCCACAGGTGTGACTTCACTTACGAAACCAACATGATGCGCAGATCCGAGAGATCTAGG
 AGAAGTTTGGGAAGCAGCCCTCAGCTGCCAGCCAGCGGCTGAAGCTCGCGGGCGGAAGAGAGCAGACGAT
 GGGTGAACCCCTCGTGGCCCTTGAGACTCTCTGGGACCATGCAAAATTAACCAACTGTGATAGCTCCCATAG
 TGAGCTCACTCATGTTGTTTCTCTGTAATCAAGAAGTGCTGGAAGAGAGGTTGATTGTGAGGCGAGTCC
 CAAAAGGGAAGCTGGAGCTGAGGCTGTTTCTTTTCTGTTCCATTATTCGAAATCTTGGACAGAGCA
 GCAGAGAAAGCTGATGGGAGTGAGAGACTCAGCAAGCCAACTGGGATCAGAGAGAGAGGGAAGGAGG
 GAGGCTCTCGCTTCAGAGCTCTGGCTGCATAGAAAGGATTCTGGTGTCTTCCCTGTTTGGCTGGCAGAGG
 GTTCCAGTGCAATTTGCAATTTGACAGCTAAATTTGACAGATTTCCCGAGCTGGCTGTCCCAATGTATTACA
 TTTGAGATGCTCCAGGCGCTCTAAGAGAATCCACCTCTCTGGCCCTGGGACATGCAAGATCTGCTACATAA
 ATTTCTGTGTTTCTTGGCAATAGCGTCATTGCCAAGTGCACATCAGTGAGGCTCTTGATCTGTTAGTCTCTC
 TTTCAACAAAGAGTGTTGTCAGAAAAGGAGAGAGAGCTGAGATCATTCAGGAGTTTGTGGGCGAGCA
 TGGAGCTCTTCTGCAAAATCTGGGCTCATAAACACCCCAAGTCCCTGTGATCAGTAGCTCCCTGGAGTT
 CCCCAGGTGAGGAGAGCAGAGTGCCAGCTTCTGAAGGGCCAGAAATTTAGCTGGATCTGCTCTTTAC
 CTGCTAGGACTTGGAAAGAGCCAGAGTGGGTGGCTGAGGCTCTCTGCTGTGAGGTATGCCCTGTGTG
 GAATTTGAGTGCTCATGGGTGGGCTCATATCAGCTGGGAGTTATTTTGATATGTAGAATGCCAGATCTTCCA
 GATTAGGCTAAATGTAATGAAACCTCTTAGGATATCTGTGGAGCATCAGTTTGGGAAGAAATTTGAAATTA
 CTTGCAAGAAAAAGTATGTCTCACTTTTGTAAATGTGCTGCTCATTGACCTGGGAAAAATGAAAAAAA
 AATAAGCAATGGTAAGACCTTTAAAAAAAAGAAAAAAAAGAAAAAAAAGAAAAAAAAGAAAAAAA

FIGURE 36

MSRPGTATPALALVLLAVTLAGVGAQGALEDPDYYGQEIWSREPYARPEPELETFSPLP
AGPGEWERRPQEP RP PKRATKPKKAPKREKSAPEPPPGKHSNKKVMRTKSSEKAANDHS
VRVAREDVRESCPLGLETLKITDFQLHASTVKRYGLGAHRGRNLQAGINENDFYDGAWCA
GRNDLQQWIEVDARRLTRFTGVITQGRNSLWLSDWVTSYKVMVSNDSHTWVTVKNGSGDMIF
EGNSEKEIPVLNELPVPVMVARYIRINPQSWFDNGSICMRMEILGCPLDPDNYYHRRNEMTT
TDDLDFKHNYKEMRQLMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHPGEHEVGEPEF
HYIAGAHGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLPSLNPBGYEKAYEGG
SELGGWSLGRWTHDGDIDNNFPDLNTLLWEAEDRQNVPRKVPNHYIAIPEWFLSENATVAA
ETRAVIAWMEKIPFVLGGNLQGGELVVAYPYDLVRS PWKTEHTPTPDDHVFRWLAYSAST
HRLMTDARRRVCHTEDFQKEEGTVNGASWHTVAGSLNDFSYLHTNCFELSIYVGCDKYPHES
QLPEEWENNRESLIVFMEQVHRGIKGLVRDSHGKIPNAIISVEGINHDIRTANDGDYWRLL
NPGEYVVTAKAEGFTASTKNCMVGYDMGATRCDFTLSKTNMARIREIMEKFGKQPVSLPARR
LKLGRKRRQRG

FIGURE 37

CTAAGAGGCAAGATAGAGGCCCGGCTCTCATTCTCTAGCCCTTCTGTCTTCTCCTTGCCCAAGCTGCAGGGG
 ATTTGGGGGATGTGGGACCTCCAATCCCAGCCCCGGCTCAGCTCTTCCCAGGTGTTGACTCCAGCTCCAGC
 TTCAGCTCCAGCTCCAGCTCGGGCTCCAGCTCCAGCCGACGCTTAGGCAGCGGAGGTTCTGTGTCCAGTTGTT
 TTCCAATTTCCACGGCTCCGTGGATGACCGTGGGACCTGCCAGTGCTCTGTTCCTCCGACAGACACACCTTTC
 CCGTGGACAGATGGAAACGCTTGGAAATTCACAGCTCATGTTCTTCTCAGAAAGTTTGAGAAAGAACTTCTAA
 GTGAGGGAATATGTCCTAATTAATTAAGTGTGTATGAAAAAACTGTTAAACCTAACTGTCGGAATTGACATCAT
 GGAGAAGGATACCACTTCTTACACTGAACTGGACTCAGCTGATCAAGGTAGAAGTGAAGGAGTGAAGAAAC
 TGGTCATACAGCTGAAGGAGAGTTTGGTGGAGCTCAGAAATTTGTAGCAGCTGGAGGTGGAGATAGAATAT
 ATGACTCTCTTGGTAGAGAACCTTGAGACACTAGACAAAAACAATGTCCTTGCCATTGCCGAGAAATCGTGGC
 TCTGAAGACCAAGCTGAAAGAGTGTGAGGCCCTAAAGATCAAAACACCCCTGTCGTCCACCTCCTCCCACTC
 CAGGAGCTGTGGTCTGTTGGTGTGGTGAACATCAGCAACCCCTCTGTGGTTGAGCTCAACTGGAGAGGGTTT
 TCTTATCTATATGGTGTCTGGGGTAGGGATTACTCTCCCCAGCTTCCAAACAAAGGACTGTATGGGTGGCGCC
 ATTTGAATACAGATGGGAGACTGTTGGAGTATTATAGACTGTACACACACTGGATGATTGGCTATTGATATATA
 ATGCTCGAGAGTTGCGGATCACCTATGGCCAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACCTCAAC
 ATGTACAACACCGGGAATATTGCCAGAGTTAACTGACCACCAACACGATTGCTGTGACTCAAACTCTCCCTAA
 TGCTGCCTATAATAACCGCTTTTCATATGCTAATGTTGCTGGCAAGATATTGACTTTGCTGTGGATGAGAAATG
 GATTGTGGGTATTATTCAACTGAAGCCAGCACTGGTAACATGGTGATTAGTAACTCAATGACACCACTT
 CAGGTGCTAAACACTTGGTATAACCAAGCAGTATAAACCATCTGCTTCAAGCCCTTCATGGTATGTGGGGTTCT
 GTATGCCACCCGTACTATGAACACCAAGAACAGAGAGATTTTTTACTATTATGACACAACACAGGGAAGAGG
 GCAAACTAGACATTGTAATGCATAAGATGCAGGAAAAAGTGCAGAGCAATTAACCTATAACCTTTTGACCAAGAA
 CTTTATGTCTATAACGATGGTTACCTCTGAATATGATCTTCTGCTCTTGACAGAGCCCCAGTAAAGCTGTTTA
 GGAGTTAGGGTGAAGAGAAAAATGTTTGTGAAAAAATAGCTCTTCCACTTACTTAGATATCTGCAGGGGTGT
 CTAAAAGTGTGTTCACTTTTGCAGCAATGTTTAGTGCATAGTTCTACCACACTAGAGATCTAGGACATTTGTCT
 TGATTTGGTGAGTCTCTTGGCAATCATCTGCCCTCTCAGGCGCAATTTGCAATAAAGTCTGTCTAGGGTGGGA
 TTGTCAGAGGTCTAGGGGCACTGTGGGCTAGTGAAGCCCTACTGTGAGGAGGCTTCACTAGAAGCTTAAATTA
 GGAATTAAGGAACCTAAAACTCAGTATGGCTCTAGGGATTCTTTGTACAGGAAATATTGCCCAATGACTAGCT
 CTCATCCATGTAGCACCCTAATCTTCCATGCTGGAAGAACTGGGGACTTAGTTAGGTAGATTAATATCT
 GGAGCTCTCGAGGGACCAATCTCCAACCTTTTTTCCCTCACTAGCACCTGGAATGATGCTTTGTATGTG
 CAGATAAGTAAATTTGGCATGCTTATATATTCTACATCTGTAAGTGCTGAGTTTATGGAGAGAGGCCCTTTT
 ATGCAATTAATTTGTACATGGCAATAAATCCAGAAGGATCTGTAGATGAGGCACCTGCTTTTCTTCTCTC
 ATTGTCACCTTACTAAAAGTCAGTAGAATCTTACCTCATAACTCTCTCCAAAGGACGCTCAGAAGATTAG
 AACAGACTTACTAACCAATTCACCCCCACCAACCCCTTCTACTGCCTACTTAAAAAATTAATAGTTTT
 CIATGGAAGTATCAAGATTAGAAAAATTAATTTTCTTTAATTTCAATTGAGCTTTTATTACATGACTCTA
 AGACTATAAGAAAACTGATGGCAGTGACAAAGTGCTAGCAATTTATGTTATCTAATAAGACCTTGAGCATA
 TGTGCAACTATGAGTGTATCAGTTGTTGCAATGTAATTTTTGCCTTTGTTAAGCTGGAACCTTGAGCAAT
 GAAAAATTTAATTTTTTTCTAGGACGAGCTATAGAAAACTATTGAGACTCTAGTAAATCATGTGACGATAGT
 TGGAAACCTTGTGGTGTATGTGTGCTTCTGTCTTTGAATGACTTTATCATCTAGTCTTTGTCTATTT
 TCCTTTGATGTTCAAGTCTAGTCTATAGGATTGGCAGTTTAAATGCTTTACTCCCCCTTTTAAATTAATGAT
 TAAATGTGCTTTGAAAAAAGAAAAAAGAAAAAAGAAAAA

MRPGLSFLALLFFLGQAAGDLGDVGPPIPSPGFSFSPGVDSSSSFSSSSRSGSSSSRLGS
GGSVSQFLFSNFTGSVDGRGTCQCSVSLPDTTFPVDRVERLEFTHVLSQKFEKELSKVREYY
QLISVYEKKLLNLTVRIDIMEKDTISYTELDFELIKVEVKEMEKLVIQLKESFGGSSEIVDQ
LEVEIRNMTLLVEKLETLDKNNVLAIRREIVALKTKLKECEASKDQNTPVVHPPPTPGSCGH
GGVVNISKPSVVQLNWRGFSYLYGAWGRDYSQHPNKGLYWVAPLNTDGRLLLEYRYLNTLD
DLLLYINARELRITYQGSGTAVYNNMVMYNNMTGNIARVNLTTNTIAVTQTLNPAAYNNR
FSYANVAWQDIDFAVDENGLWVIYSTEASTGNMVISKLNDDTLQVLNTWYTKQYKPSASNAF
MVCGLVYATRMTNTRTEEI FYYYDTNTGKEGKLDIVMHKMQEKVQSINYNPFDQKLYVYNDG
YLLNYDLSVLOKPO

FIGURE 39

GCTCTGAAGACCAAGCTGAAAGAGTGTGAGGCCTCTAAAGATCAAACACCCCTGTCGTCCAC
CCTCCTCCCACTCCAGGGAGCTGTGGTCATGGTGGTGGTGAACATCAGCAAACCGTCTGT
GGTTCAGCTCAACTGGAGAGGTTTTCTTATCTATATGGTGCTTGGGGTAGGGATTACTCTC
CCCAGCATCAAACAAAGGNATGTATTGGGNGCGCCATTGAATACAGATGGGAGACTGTTG
GAGTATTATAGACTGTACAACCCACTGGATGATTTGCTATTGTATATAAATGCTCGAGAGTT
GCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAACA
TGTACAACACCGGNATATTGCCAGAGTTAACCTGACC

TO THE

FIGURE 40

TCTCGCAGATAGTAAATAATCTCGGAAAGGCGAGAAAGAAGCTGTCTCCATCTTGTCTGTAT
 CCGCTGCTCTTGTGACGTTGTGGAGATGGGGGAGCGTCTGGGGCTGTGCTCCATGGGGAGCT
 GGATACCATCTTTGTGTGAAGTGCCTCGTGTGGCTAGCCGATGCTGCTCTAGTGGAAAC
 AACTCCACCTGTAAC TAGATGATCTATGCACTTTTCTTGTGTTGGAGTATGTGTAGCTTG
 TGTAAATGTTGATACCAGGAATGGAAGAACAACTGAATAAGATTCTCGGATTTTGTGAGAAAG
 AGAAAGGTTGTGCTCTTGTAAACATTTTGGTTGGCTATAAAGCTGTATCTGTTTGTGCTTT
 GCTTTGGCTATGTTCTTATCTTCTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGA
 TCTTAGAGCTGCACTGCAACAATGGATTTTGGTTCTTTAAATTTGCTGCAAGCAATTGCAATTA
 TCATTGGGGCTTTCTTCTTCCAGAAGGAACTTTACAACGTGTGTGTTTATGTAGGCCATG
 GCAGGTGCCCTTTGTTTTCATCTCTACAACTAGTCTTACTATTGATTTTGCACATTCATG
 GAATGAATCGTGGGTTGAAAAATGGAAGAAGGGAACTCGAGATGTTGGTATGCAAGCTTTGT
 TATCAGCTACAGCTCTGAATTAATCTGCTGCTTTAGTTGCTATCGTCTGTTCTTTGTCTAC
 TACACTCATCCAGCCAGTTGTTTCAAGAAACAGGCGTTACATCAGTGTCAACATGCTCTCTG
 CGTTGGTCTTCTGTAATGCTATACTGCCAAAAATCCAAGAATCAACCAAGATCTGGTT
 TGTACAGCTCTTCACTAATTACAGTCTACAAATGTAATTGACATGGTCAGCTATGACCAAT
 GAACCGAAACAAATGCAACCCAGTCTACTAAGCATAATTGGGTACAAATACAACAGCAC
 TGTCCCAAGGAAGGGCAGTCACTCCAGTGGTGGCATGCTCAAGGAATTATAGGACTAATTC
 TCTTTTGTGTTGTGATTTTATTCAGCATCCGTACTTCAACCAATAGTCAAGTTAAATAA
 CTGACTTCAACAGTGAATGAACTACATTAATAGAAGTGGTGGAGCTAGAAGTGTGGATG
 ACTGGAGGATGGGAGCATGTTCCACCGAGCTGTAGATAATGAAAGGGATGGTGTCACTTACA
 GTTATCTCTTCTTTCACCTTCTGCTTTTCTGGCTTCACTTTATATCATGATGACCCTTACC
 AACTGCTCCAGGATGAACCCCTCTCGTGAGATGAAAGTCAGTGGACAGCTGTCTGGGTGAA
 AATCTCTTCCAGTTGGATTGGCATCGTGTGATGTTTGGACACTCGTGGCACCCTTGTTC
 TTACAAATCGTGATTTTGACTGAGTGTAGATGAAAGTCCCACTTTGATTATTGTC
 TTATTGAAACAGTATTTCCCACTTTTGTAAAGTTGTGTATGTTTGTCTTCCATGTAAC
 TCTCCAGTGTCTGGCATGAATTAGATTTTACTGCTGTGATTTTGTATTCTTCTTACCAG
 GTGCATGTATGTGAAGTAGAATGAATTTGCAGAGGAAAGTTTATGAATATGGTGTAGAT
 TAGTAAAGTGGCCTATTATGGGCTTATTCCTGCTCTATAGTTTGTGAATGAAGAGTAAAA
 ACAATTTGTTTACTATTAAAAATATATAGACCTTAAGCTGTTTTAGCAAGCATTAAG
 GCATTTGATGGCTGCCCTTTTGAATATTTGATGTGTTGCCCTGGCAGGTAAGTCAAGAAC
 ATGGTTTATTTTAAATTTATAAACAGTCACTTAAATGCCAGTTGTCTGAATAATCTTATA
 AGGTTTACCCTTGATACGGAATTTACACAGGTAGGAGTGTTAGTGGACAAATAGTGTAGG
 TTATGGATGGAGGTGTCGCTACTAAATGAATAACGAGTAAATAATCTTACTTGGGTAGAGA
 TGGCCTTTGCCCAACAAAGTGAAGTGTGTTGGTTGTTTAAACTCATGAAGTATGGGTTCACT
 GGAATGTTTGGAACTCTGAAGGATTAGACAAGTGTGAAAGGATAATCATGGGTAGA
 AGGAAGTGTTTTGAAGTCACTTTGAAAGTGTAGTTTGGGCCAGCAGCGTAGCTCACCCTT
 GGTAAATCCAGCATTTGGGAGCTTAAGTGGGTAGATTACTTGAGCCAGGAATTCAGACCA
 GCTTTGGCAGATGGTGAACCTGTTCTATAAAAAATATCTGGCTTTGAGCATATGCTCTGGTCT
 CAGCATGAGAGGCTAGTGAAGATTGCTGAGCCAGAGCCAAAGGTTGCAAGTGAAGCAAGTCA
 CGTCACTGCACTCTAGCTGGCACAGAGTAAGCCAAAAAATATATATATGAATCAAGG
 AGGCAAAATTTGACAGGGAAGGAAGTAAGTGCAAAACCTAGGCTTTAGTAGGCTATTAT
 ATAAAACTAGTCCAGTTCTCTCATTAAAAAATGAAGACATGAAATACAGACTTAATTA
 CTCAGATAGCTAATTTAGGAATTTCAAGTTGGCCAAATAATAGCATTTCTCTGTACATTTAA
 AAAATATTTCTATTCAAATACATGCATATTTGATTTACACCTCATAGCTGTGATTAATTAATGT
 GATGTGGATTGCTGTGTCAGCATGACCCATAAACAGGTGCAAGAAATGATGGAATGTTTT
 AGAATAAATCCTGCTTTATAGTATATACACAGTTCAAAGATGTTTAAATGCTTTTGTAT
 TTACTGGCATGTAATTTGAATATATAGATTATTGTAACCTTTCAACCTGAAATCAAGCAGT
 ATGAGAGTTTGTGTTTGTATGTGTCACTAGTGTCTAATGAAGCTTTTAAATCTCAACAT
 TCTTCTTTAAAAATATTTAATGTGAATGGAATATAACAACTCAGCTTAATTTCCCAACC
 TTATCTGTGTGTAGACATTGTATCCCAATTTTGAATGGCTGTGTTTACCTCTAAATAA
 ATGAATTCAGAGAAAAA

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MGSVLGLCSMASWIPCLCGSAPCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGME
EQLNKIPGFCENEKGVPNCNILVGYKAVYRLCFGLAMFYLLSLMLIKVKSSSDPRAAVHNG
FWFFKFAAAIAIIIGAFFIPEGTFTTVWFYVGMAGAFCFILIQVLVLLIDFAHSWNESWVEKM
EEGNSRCWYAALLSATALNYLLSLVAIVLFFVYTHPASCSENKAFISVNMLLCVGASVMSI
LPKIQESQPSRGLLQSSVITVYTMYLTSAMTNEPETNCNPSSLIIGYNTTSTVPKEGQSV
QWWHAQIIIGLILFLLCVFYSSIRTSNNSQVKNLTLTDESTLIEDGGARSDDGSLEDGDDVH
RAVDNERDGVITYSYFFHMLFLASLYIMMTLTNWSRYEPSREMKSQWTA VVVKISSWIGI
VLYVWTLVAPLVLNDRFD

FIGURE 42

GCGAGAAAGAAGCTGTCTCCATCTTGTCTGTATCCCCTGCTTCTTGNGACGTTGTGGAGAT
GGGGAGCGTCCCTGGGGCTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCC
CCGTGTTTGCTATGCCGATGCTGTCCTAGTGGAACAANTCCACTGTAAGTAGATTGATCTA
TGCACTTTTCTTGCTTGTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAG
AACAACTGAATAAGATTCCCTGGATTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATT
TTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTTCT
CTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGAT
TTTGGTTCTTTAAATTGCTGCAGCAATTGCAATTATTATTGGGGC

FIGURE 43

GTTATTGTGAACTTTGTGGAGATGGGAGGTCNTGGGGCTGTGTTCCATGGCGAGCTGGATAC
CANGTTTGTGTGGAAGTGCCCCGTGTTTGTATGCCGATGCTGTCCTAGTGGAACAANTCC
ACTGTAATTAGATTGATNTATGCACTTTTNTTGTCTTGTGGAGTANGTGTAGCTTGTGTAAT
GTTGATACCAGGAATGGAAGAACAACCTGAATAAGATTCTGGATTTTGTGAGAATGAGAAAG
GTGTTGTCCTTGTAAACATTTTGGTTGGCTATAAAGCTGTATATNGTTTGTGCTTTGGTTTG
GCTANGTTCTATNTTCTTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAG
AGCTGCAGTGACAATGGATTTTGGTTTTTTAAATTTGCTGCAGCAATTGCAATTATTATTG
GGGC

AAGAAGCTGTCTCCACTTGTCTGTATCCGCTGCTCTTGTGAACGTTNTGGAGATGGGGAGC
GTCCTTGGGGTTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCCCCGTGTT
TGCTATGCCGATGCTGTCTAGTGGAAACAACCTCCACTGTAAC TAGATTGATCTATGCACTT
TTCTTGCTTGTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAGAACAACT
GAATAAGATTCCTGGATTTTGTGAGAATGAGAAAGGTGTTGCCCTTGTAACATTTTGGTTG
GCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCATATGTTCTATCTTCTCTCTTTA
CTAATGATCAAACTGAAGAGTAGCAGTACTGAGCTAGCTGCAGTGCACAATGGATTTTGGTT
CTTTAAATTTGCTGCAGCAATTCGAATTATATTGGGGC

FIGURE 45

GCTGTCCTTAGTGGAACAANTCCAACCTTGTAACCTTGGATTGATCTATGCACATTTTTCCTTG
CTTGTTGGAGTATGTGTAGCTTTGTGTAATGTTGTTCCAGGATTGGANGAACAACTGAATA
AGATTCCCTGGATTTTTGTGAGAATGAGAAAGGTGTTGTCCCCTTGTAACATTTTTGGTTGGC
TATAAAGCTGTATATCGTTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTTCTCTTTACT
AATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTTGGTTCT
TTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGCATTCTTCATTCCAGAAGGAACTTTT
ACAACTGTGTGGTTTTATGTAGGCATGGCAGGTGCCTTTTGTTCATCCTCATACTAGT
CTTACTTATTGATTTTGCACATTCATGGAATGAATCGTGGGTGAAAAATGGAAGAAGGGA
ACTCGAGATGTTGGTATGCAGCCTTGTTATCAGCTACAGCTCTGAATTATCTGCTGTCTTTA
GTTGCTATCGTCCTGTTCTTTGTCTACTACACTCATCCAGCCAGTTGTTTCAGAAAAACAAGC
GTTTCATCAGTGTCACATGCTCCTCTGCGTTGGTGCTTCTGTAATG

FIGURE 46

CTCGGGCGCGCAGGCGAGCTCGGTTTGCCTGCGATTGAGCTCGGGGTGCGGGCGCGGCCGCGGCTCTCCAAT
GGCAAAATGTGTGTGGCTGGAGGCGAGCGCAGGCTTTCGGCAAAGGCAGTGCAGTGTTCGACACCGGGGCGAG
TCCCTGTAAACGAGATAAAAGCAAAACATTATTAAAGCTGTATTACGAGGGAGCGCCCGGGCGGGGCTGTCCG
ACTCCCCCGGCAACATTTTGGCTCCCTCAGCTCCGAGAGGAGGAGAAAGAAAGCGGAAATGAGGAGCAGATTAC
GTCCGTTTCAGCGCAANGTGCACCTGTATCGATGGCCCTCCTGAATTTATCAGATATTTGATTTAGTCGATGCC
CCCTGGTTTGTGTGTACGCACACACAGCTGCACAAAGGCTCTGGCTCGCTCCCTCCCTCGTTTCGAGCTCC
TGGGCGAATCCACATCTGTTTCAACTCTCCGCGAGGGCGAGCAGGAGCAGAGATGTGTGCAATTCGCGAGTG
AAGAGGCGAGGGGAAAAAGAAACAAAGCCACAGAGCGCACTTGAGACTCCGCGATCCCAAAGAGCAGCAAGAT
CAGCAAAAAAGAAAGATGGGCCCGCCGAGCCTCGTGTGTGCTGTCTGTCCGCACTGTGTTCTCCCTGTCTGGG
TGGAAAGCTCGGCTTCTGTGTCAGCACCACCGCTGAAAGGCGAGGTTTCAGAGGGACCGCAGGAACATCCGCCCA
ACATCATCTCGTGTGCTGACGGACAGCCAGGATGTGAGAGCTGGGTTCCATGCAAGGTGATGAACAGACAGCCGCGC
ATCATGGAGCAGGGCGGGGCGCACTTCATCAACGCCCTGTGACCAACACCCATGTGCTGCCCTCAGCTCCTC
CATCTCCTGAGTACGTGCACAAACCAACACCTACACCAACATGAGAACTGCTCCTGCCCTCCTCGG
AGGCACAGCACGAGAGCGCGCACTTTCGCGTGTACCTCAATAGCACTGGCTACCGGACAGCTTCTTCGGGAAG
TATCTTAATGAATACAACGGCTCCTACGTGCCACCGGCTGGAAGGAGTGGTGGGATCCTTTAAAACTCCCG
CTTTTATAACTACAGCTGTGTGCGAACGGGTTGAAAGAGAGACGGCTCCGACTACTCAAGGATTACCTCA
CAGACCTCATCAACATGACAGCGTGAAGCTTCTTCGCGAGCTCCAAAGAAGATGACCCGCAAGCCGCTCTCT
ATGGTCATCAGCCATGACGCGCCCGCCAGCGCTGAGGATTCAGCCCAACATATTCAGCGCTCTTCCCAAACGC
ATCTCAGCACAATCAGCGCGAGCTACAACTACGCGCCCAACCCGGACAAACATGGATCATGGCTACACGGGG
CCATAGGCGCCATCCACATGGAATTCACCAACATGCTCAGCGGAAGCGCTTGCAGACCTCATGTCCGTTGGAC
GACTCCATGAGACGATTTCACACATGCTGGTTGAGACGGGCGAGCTGGACACACAGCTACATCGTATACACCGC
CGACAGGCTTACCACCTCGGCGAGTTTGGCTGGTGAAGGGAAATCCATGCCATGATGTTTGAATCAGG
TCCGCTTCTACGTGAGGGGCGCCACAGCTGGAAGCGGCTGTCTGAATCCCACTCGCTCCTCAACTGAGCTG
GCCGCCACCATCTGGACATTCAGGCTTGGACATACCTGCGGATGAGGAGGAAATCCATCTCAAGCTGT
GGACAGCGGAGCGCGGTGAATCGGTTTCACTTGAAAAAGAGATGAGGCTGCGCGGAGTCTCTTCTGTGTG
AGAGAGGCAAGCTGCTACAAGAGAGACAAATGACAAGTGGAGCGCCAGGAGGAGAACTTTCGCCCAAGTAC
CAGGCTGTGAAGGACCTGTCTCAGCGTGTGATGATACGAGCGGCTGTGAGCAGCTGGGACAGAAGTGGCAGT
TGTGAGGAGCGCCACCGGGAAGCTGAAGCTGCATAAGTGCAGGGGCCCTGCGCTGGGCGGACAGCAGCC
TCTCCACCTCTGTCGCCAAGTACTACGGGCGAGGCGAGGCTGCACTGTGACACGGGGGACTACAAGCT
AGCTTGGCGGAGCGCGGAAATAACTTTCAGAAAGAAAGTACAAGGCCACTATGTTCCGCACTCGCTCCACTCG
CTCAGTGGCCATCGAGCTGACCGGAGGCTGTACACCTAGGCTGGGCTGATGCGGCCAGCGCCGAAACCTCA
CGAAGCGCACTGGCCAGGCGCCCTGAGGACCAAGATGACAAGATGTTGGGACTTTCAGTGGCACTGGAAGC
CTTCCGCACTACTCAGCGCCCAACCCCATTAAGTGAACATCGGTGCTACATCTAGAGAAGCAGACAGTCCA
GTGTGAGCTGGACCTGTACAAGTCCCTGCGAGCTGGAAAGACCAAGCTGCACATGCACACGACCACTGAA
CCCTGCAGAACAAATTAAGAACCTGAGGGAAGTCCGAGGTCACCTGAAGAAAAAGCGGCGCAGAAGATGTGAC
TGTCACAAATCAGCTACCAACCCGACACAAAGGCGGCTCAGCAGCAGGCTCGAGTCCGTTCTTCAG
GAAGGCGCTGCAAGAGAAGGACAGGTGTGGCTGTTTCGGGAGCAGAAGCGCAAGAAAGAACTCCGAGGCTCG
TCAAGCGGCTGCAGAACACGACACGTGAGCATCGCAGGCTCAGGCTGTTCCACCAACGACCACTGAG
CAGAGCGCGCTTCTGCGACATCGGGGCTTCTGTGCTGCACGCGCCACACATACACAGCTACTGCTGCAT
GAGGACCATCAATGAGACTCACAAATTCCTCTCTGTGAATTTGCACTGGCTCTCAGATGACTTGTATCTCA
ACACAGACCCCTACAGCTGATGAATGACGTGAACACATGGACAGGAGTGTCTTCAACAGCTCAGGCTACAG
CTCATGAGGCTGAGGAGCTGCAAGGGTTACAAGCAGTGAACCCCGGATCGAACACATGGACTCGGATGAGG
AAGCTTATGACCAATACGCGACTTTCAGCTGCAAAAGTGGCGCAAAATGAAGAGACCTTCTTCCAAATCCTG
GCAACTCTGGGAAGGCTGGGAAGGTTAGAAACCAACAGAGGTGGACCTCCAAAGACATAGAGGCATCACTGA
CTGCACAGGCAATGAAACCACTGTGGGTGATTTCACAGACAGCTGTGCTATTTCCGAGGAGGAGCTGAGAAGC
AAGCAGCAGCTCTCAGTCAACATGACAGATTCTGGAGGATAACCGACAGGAGCAGAGATAACTTCAGGAAGTCC
ATTTTTCGCCCTGCTTTTGGATTGATATACCTCACCAGCTGCACAAAGTGCATTTTCGTATCAAAAGTCT
ACCACTAACCTCCCCAGAAGCTCAAAAGGAAAAACGAGAGAGCGGAGGAGAGATTTCTTGGAAATTTTC
TCCAAAGGGGAAAAAGTCATTGGAATTTTAAATCATAGGGGAAAAAGCATGCTCTTAACTAACTCTTATTCTT
TTGGTTTGTCAAAAGAGAACTAAGAAGCAGGACAGAGGCAACGCTGGAGAGGCTGAAAAACAGTGCAGAGAGC
TTGTGCAATGAGTACAGTACAAAGAGATGACATTACCTAGCATAAACCCTGGTTGCTCTGAAAGAA
CTGCCTCATTTGATATATGTGACTATTACATGTAATCAACATGGGAATTTTAGGGGAGCACTATAAGAAAT
CCCAATTTTCAGGAGTGGTGTCAATAAACGCTCTGTGGCAGTGTAAAGAAAA

FIGURE 47

MGPPSLVLCLLSATVFSLLGGSSAFLSHHRLKGRFQRDRRNIRPNIILVLTDDQDVELGSMQ
VMNKTRRIMEQGGAHFINAFVTTMCCPSRSSILTGKYVHNHNTYTNNENCSSPSWQAQHE
RTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWVGLLKNSRFYNYTLCRNGVKEKHGSD
YSKDYLTDLITNDSVSFFRTSKKMYPHRPVLMVISHAAPHGPEDSAPQYSRLFPNASQHITP
SYNYAPNPDKHWIMRYTGPMKPIHMEFTNMLQRKRLQTLMSVDDSMETIYNMLVETGELDNT
YIVYTADHGYHIGQGLVKGKSMPYEFDIRVPFYVRGPNVEAGCLNPHIVLNLIDLAPTILDI
AGLDIPADM DGKSILKLLDTERPVNRFLKKKMRVWRDSFLVERGKLLHKRDNDKVDAQEEN
FLPKYQVRKDL CQRAEYQTACEQLGQKWQCVEDATGKLKLHKCKGPMRLGGSRALSNLVPKY
YGQGSEACTCDSGDYKLSLAGRRKKLFKKKYKASYVRSRSIRSAIEVDGRVYHVGLGDAQ
PRNLTKRHWPGAPEDQDDKDGDFSGTGGLPDYSAANPIKVTHRCYILENDTVQCDDL DYKS
LQAWKDHKLHIDHEIETLQNKIKNLREVGRHLKKRPEECDCHKISYHTQHKGRLKHRGSSL
HPFRKGLQEKD KVVLLREQKRKKKLRKLLKRLQNNDTCSMPGLTCFTHDNQHWQTAPFWTLG
PFCACTSANNNTYWC MRTINETHNFLFCEFATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQL
HVQLMELRSCKGKYQCNPRTNRNMDLDGGSYEQYRQFQRRKWPEMKRPSSKSLGQLWEGWEG

FIGURE 48

AACAAAGTTCAGTGACTGAGAGGGCTGAGCGGAGGCTGCTGAAGGGGAGAAAGGAGTGAGGA
GCTGCTGGGCAGAGAGGGACTGTCCGGCTCCCAGATGCTGGGCCCTCCTGGGGAGCACAGCCC
TCGTGGGATGGATCACAGGTGCTGCTGTGGCGGTCTGCTGCTGCTGCTGCTGCTGGCCACC
TGCCTTTTCACGGACGGCAGGACTGTGACGTGGAGAGGAACCGTACAGCTGCAGGGGGAAA
CCGAGTCCGCCGGGCCCCAGCCTTGGCCCTTCCGGCGGCGGGGCCACCTGGGAATCTTTCACC
ATCACCGTCATCCTGGCCACGTATCTCATGTGCCAATGTGGGCCTCCACCACCACCACCAC
CCCCGCCACACCCCTCACCACCTCCACCACCACCACCACCCCCACCGCCACCATCCCCGCCA
CGCTCGCTGAGGGCTGCTGTCGCCGGTGCCTGTGGACAGCAGCTGCCCCCTGCCCTCCCATCTG
TTCCAGGACAAGTGGACCCCATGTTTCCATGTGGAAGGATGCATCTCTGGGGTGAACGAGG
GGAACAATAGACTGGGGCTTGCTCCAGCTGCATTTGCATGGCATGCCCCAGTGTAATATGGC
AGCAGAGAATGGAGGAACACTGGGTCTGCAGTGTGAAGGGTTTGGGGAGTGGAGAGCAAGG
GTGCTCTTTTCGGGGCTGGACAGCCCGTCTTGTGACAGTGACTCCAGTGAGCCCCAGAAATG
ACAAGCGTGTCTTGGCAGAGCCAGCACACAAGTGGATGTGAAGTGCCCGTCTTGACCTCCTC
ATCAGGCTGCTGCAGGCCTCTGGCGGGCAGGGCACTGGGAGAGGCCCTGAGAATGTCCTTTT
GGTTTGGAGAAGGCAGTGTGAGGCTGCACAGTCAATTATCGGTGCCTTAGTCCAAGAAAAT
AAAAACCACTAAGAAGCTTTAAAAAAAAAAAAAAAAAAAAA

FIGURE 49

MLGLLGSTALVGWITGA AVAVLLLLLLLATCLFHGRQDCDVERNRTAAGGNRVRAQWPWFER
RRGHLGIFHHHRHPGHVSHVPNVGLHHHHHPRHTPHHLHHHHHPHRHHPRHAR

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FIGURE 50

GGCGGCTGCTGAGCTGCCTTGAGGTGCACTGTTGGGGATCCAGAGCCATGTCGGACCTGCTA
CTACTGGGCTGATTGGGGCTGACTCTCTTACTGCTGCTGACGCTGCTGGCCTTTGCCGG
GTACTCAGGGCTACTGGCTGGGGTGGAAAGTGAGTGCTGGGTACACCCCATCCGCAACGTCA
CTGTGGCCTACAAGTTCACATGGGGCTCTATGGTGAGACTGGGCGGCTTTTCACTGAGAGC
TGCAGCATCTCTCCAAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCCATAGGTGCC
CCCTGATAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAGGTGAGGAATCGCCCTCCC
CTGAGCTCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAGC
CATGTGGTGACAGCCACCTTCCCCTACACCACCATTTCTGTCCATCTGGCTGGCTACCCGCCG
TGTCCATCCTGCCTTGGACACCTACATCAAGGAGCGGAAGCTGTGTGCCATCCTCGGCTGG
AGATCTACCAGGAAGACCAGATCCATTTTCATGTGCCCACTGGCACGGCAGGGAGACTTCTAT
GTGCCGTGAGATGAAGGAGACAGAGTGGAAATGGCGGGGGCTTGTGGAGGCCATTGACACCA
GGTGGATGGCACAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGAAGTGAGCC
CTGGCAGCCGGGAGACTTCAGCTGCCACACTGTCACTGGGGCGAGCAGCCGTGGCTGGGAT
GACGGTGACACCCGACGCGAGCACAGCTACAGCGAGTCAGGTGCCAGCGGCTCCTCTTTTGA
GGAGCTGGACTTGGAGGGCGAGGGGCCCTTAGGGGAGTCACGGCTGGACCCTGGGACTGAGC
CCCTGGGACTACCAAGTGGCTCTGGGAGCCCACTGCCCCTGAGAAGGCAAGGAGTAACCC
ATGGCCTGCACCTCCTGCAGTGCAGTTGCTGAGGAACTGAGCAGACTCTCCAGCAGACTCT
CCAGCCCTCTTCTCCTTCTCTGGGGGAGGAGGGTTCTTGAGGGACCTGACTTCCCCTGC
TCCAGGCCTCTTGCTAAGCCTTCTCCTCACTGCCCTTAGGCTCCAGGGCCAGAGGAGCCA
GGGACTATTTTCTGCACAGCCCCAGGGCTGCCGCCCTGTTGTGTCTTTTTTTCAGACTC
ACAGTGGAGCTTCCAGGACCCAGAATAAAGCCAATGATTTACTTGTTCACCTGAAAAAAA
AAAAA

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FIGURE 51

MSDLLLLGLIGGLTLLLLLTLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGLYGETGR
LFTESCSISPKLRSIAVYYDNPHMVPPDKRCRCAVGSI LSEGEESPSPELIDLYQKFGFKVFS
FPAPSHVVTATFPYTTILSIWLATRVRVHPALDTYIKERKLCAYPRLEIYQEDQIHMCPLAR
QGDFYVPEMKETEWKRWGLVEAIDTQVDGTGADTMSDTSSVSLEVSPGSRETSAAATLSPGAS
SRGWDDGDTRSEHSYSESASGSSFEELDLEGEGPLGESRLDPGTEPLGTTKWLWEPTAPEK
GKE

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FIGURE 52

CCGCGGGAACGCTGTCCTGGCTGCCGCCACCCGAACAGCCTGTCCTGGTGCCCCGGCTCCCT
GCCCCGCGCCAGTCATGACCCTGCGCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCT
GCTGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGA
CCCTCCAAGTGGAGACCCTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGA
GACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCT
GACCAGAGACCCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGA
GTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTTCTCACTTGGCCTAT
GGAAAACGGGGATTTCACCATCTGTCCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCT
GATTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGGGCATTTTGCCTCTGGTAG
GGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCACCTATACAGAAAGGCCAAT
AGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAAATTA
ATAAATAATAAATTTTAAAAAAGCTTAAAAAAAAAAAAAAAAAAAA

MTLRPSLLPLHLLLLLLLLSAVCRAEAGLETESPVRTLQVETLVEPPECPAEPAFGDTLHI
HYTGSVLVDGRIIDTSLTRDPLVIELGQKQVIPGLEQSLDMCVGEKRRAIIPSHLAYGKRGF
PPSPADAVVQYDVELIALIRANYWLKLVKGILPLVGMAMVPALLGLIGYHLYRKANRPKVS
KKKLKEEKRNKSKKK

FIGURE 54

CCCGGGAACGTGTTCTGGCTGCCGCACCCGAACAGCCTGTCTGGTGCCCCGGCTCCCTGC
CCCGCGCCAGTCATGACCCCTGCGCCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCTGC
TGCTCAGTGCGGCGGTGTGCCGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGACC
CTCCAAGTGAGACCCCTGGTGGAGCCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGAGA
CACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCTGA
CCAGAGACCCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGAGT
CTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTTCTCACTTGGCCTATGG
AAAACGGGGATTTCCACCATCTGTCCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCTGA
TTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGGGCATTCTTGCCTCTGGTAGGG
ATGGCCATGGTGCCACCCCTCCTGGGCCTCATTTGGGTATCACCTATACAGAAAGGCCAATAGA
CCCAAAGTCTCCAAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAAATAATA
AATAATAAATTTTAAAAAACTTA

FIGURE 55

CCGAAAGTCCCGTCCGGACCCCTCCAAGTGGAGACCCCTGGTGGAGCCCCCAGAACCATGTGCC
GAGCCCGCTGCTTTTGGAGACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACG
TATTATTGACACCTCCCTGACCAGAGACCCTCTGGTTATAGAAGCTTGGCCAAAAGCAGGTGA
TTCCAGGTCTGGAGCAGAGTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATT
CCTTCTCACTTGGCCTATGGAACCGGGATTTCACCACCTCTGTCCAGCGGATGCAGTGGT
GCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAACACTACTGGCTAAAGCTGGTGAAGG
GCATTTTGCCTCTGGTAGGGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCAC
CTATACAGAAAGGCCAATAGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAA
CAAGAGCAAAAAGAAATAATAATAATAAATTTAAAAAACTTAAAA

FIGURE 56

CTGCTGCATCCGGGTGTCTGGAGGCTGTGGCCGTTTTGTTTTCTTGGCTAAAAATCGGGGGAG
 TGAGGCGGGCCGGCGCGGGCGACACCGGCTCCGGAACCACTGCACGACGGGGCTGGACTG
 ACCTGAAAAAAATGCTGGAATTTCTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGG
 GAAAAGCGCAATATTTGCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGAT
 TATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGATTTCAACCACTCATACCATGCCT
 GTGGTGTATTAGCAACCATAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGA
 GGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGG
 TTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTTATGTTG
 CTAAGAAAAAGACATAGTATACCCTGGAATTGCTGTATTTTTCCAGAATGCCTTCATCTTT
 TTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGACTTATGCGAGTGAACACATCTGAT
 TTCCACAGCACAAACAGCCCTGCATGGGTTTGTGTTTTTTTTACTGCTCACTCCCAACCTT
 TTGTAATGCCATTTTCTAACTTATTTCTGAGTGTAGTCTCAGCTTAAAGTTGTGTAATACT
 AAAATCACGAGAACACCTAAACAACAACCAAAAATCTATTGTGGTATGCACCTTGATTAACCT
 ATAAAATGTTAGAGGAACTTTCACATGAATAATTTTTGTCAAATTTTATCATGGTATAATT
 TGTAAAAATAAAAGAAATTACAAAAGAAATTATGGATTTGTCAATGTAAGTATTTGTGATA
 TCTGAGGTCCAAAACCACAATGAAAGTGCTCTGAAGATTTAATGTGTTTATTCAAATGTGGT
 CTCTCTGTGTCAAATGTTAAATGAAATATAAACATTTTTAGTTTTTAAATATTTCCGTGG
 TCAAAATCTTCTCACTATAATTGGTATTTACTTTTACCAAAAATCTGTGAACATGTAAT
 GTAACCTGGCTTTTGAGGGTCTCCCAAGGGTGAGTGGACGTGTTGGAAGAGAGAAGCACCAT
 GGTCCAGCCACCAGGCTCCCTGTGTCCCTTCATGGGAAGGCTTCCGCTGTGCCTCTCATT
 CCAAGGGCAGGAAGATGTGACTCAGCCATGACACGTGGTTCTGGTGGGATGCACAGTCACTC
 CACATCCACCACTG

FIGURE 58

TTCTTTGGCTAAAAATCGGGGGAGTGAGGCGGGCCGGCGCGCGACACCGGGCTCCGGAACC
ACTGCACGACGGGGCTGGACTGACCTGAAAAAAATGTCTGGATTCTAGAGGGCTTGAGATG
CTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTAC
TATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGAT
TTCAACCACTCATACCATGCCTGTGGTGTATAGCAACCATAGCCTTCCTAATGATTAATGC
AGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTGCTCTGGGTCAACAGGTG
CTCGCATTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGG
ATTCTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGCTGTATT
TTCCAGAATGCCTTCATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGC

FIGURE 59

TGGACGGACCTGAAAAAATGTTTGGATTNTAGAGGNTTGAGATGTTGAGATGCATGAC
TGGGGGAAAAGCGCAAATACTATTGCTTCCATTGCTGCTGGTGANTATTTTTTACAGGCTG
GTGGATTATCATAGATGCAGNTGTTATTTATCCCACCATGAAAGATTTCAACCANTCATACC
ATGCCTGTGGTGTTATAGCAACCATAGCCTTCNTAATGATTAATGCAGTATCGAATGGACAA
GTCCGAGGTGATAGTTACAGTGAAGGTTGTTTGGGTCAAACAGGTGCTCGCATTTGGCTTTT
CGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTGGAGGTT
ATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGNTGTATTTTCCAGAATGCCTTC
ATCTTTTTTGGAGGGCTGGTTTTTAAGTTGGCCGCACTGAAGANTTATGGCAGTG

FIGURE 60

GGACACCGGGTTCCGGACCAATGCANGACGGGTGGANTGACCTGAAAAAATGTTTGGATT
TTTAGAGGGCTTGAGATGNTCAGAATGCATTGACTGGGGAAAAGCGCAATANTATTGCTTT
CCATTGCTGCTGGTGTACTATTTTTTACAGGGTGGTGGATTATCATAGATGCAGCTGTTATT
TATCCCACCATGAAAGATTTNAACCACTCATACCATGCCTGTGGTGTATAGCAACCATAGC
CTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTT
GTTTGGGTCAAACAGGTGNTCGCATTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATTT
CTGATTGNATTCTATGCGGATTCTTCTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTAT
ACCTTGGAATTNCTNTATTTTTCCAGAATGCC

TGTTC:tttG660

TAGAGGGCTTGAGATGCTCAGAAATGCATTGACTGGGGGGAAAAGCGCAATANTATTGCTTCC
ATTGNTGNTGGTGTANTATTTTTTTACAGGCTGGTGGATTATNATAGATGACGCTGTTATTT
ATCCACCATGAAGATTNNAACCANTCATACCATGCCTGTGGTGTTATAGCAACCATAGCC
TTCTAATGATTAATGCGATATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTG
TTTGGGTCAAACAGGTGNTNGCATTTGGCTTTTNGTTGGTTTCATGTTGGCCTTTGGATCTN
TGATTGCAATTATGTGGATTNTTTTGGAGGTTATGTTGCTAAAGNAAAAGACATAGTATAC
CCTGT

FIGURE 62

GGGAGGCTGTGNCCGTTTGTGTTTTNTTGGCTAAAATCGGGGAGTGAGGCGGCCCGGCGCGG
CGNGACACCGGGTTCCGGGAACCATTCACGACGGGGTGGACTGACCTGAAAAAATGTTTG
GATTTNTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGAAAAGCGCAATACTATT
GCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGT
TATTTATCCCACCATGAAAGATTTCAACCACTCATACCATGCCTGTGGTGTATAGCAACCA
TAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAA
GGTTGTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTGGTTTCATGTTGGCCTTTGG
ATNTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTTATGTTGCTAAAGAAAAGACATAG
TATACCTGGAATTGCTGTATTTTTCCAGAATGCCTTCATNTTTTTTGGAGGGCTG

FIGURE 63

CGACGCCGGCGTCA**ATG**TGGCTTCCGCTGGTGCTGCTCCTGGCTGTGCTGCTGCTGGCCGTCC
TCTGCAAAAGTTTACTTTGGGACTATTTCTCTGGCAGCTCCCCGAATCCTTTCTCCGAAGATGTC
AAACGGCCCCCAGCGCCCTGGTAACTGACAAGGAGGCCAGGAAGAAGGTTCTCAAAACAGC
TTTTTCTGACCCAAACCAAGTGCCGGAGAAGCTGGATGTGGTGGAATTTGGCAGTGGCTTTGGGG
GCTTGGCTGCAGCTGCAATTTAGCTAAAGCTGGCAAGCGAGCTGGTGGTGGGAACAACAT
ACCAAGGCGAGGGGCTGCTGTCAATACCTTTGGAAAGAATGGCCCTTGAATTTGACACAGGAAT
CCATTACATTTGGCGTATGGAAGAGGGCAGCATTTGGCCGTTTTATCTTTGGACCAGATCACTG
AAGGCGAGCTGGACTGGGCTCCCCGTCTCTCTCCTTTTGACATCATGGTACTGGAAGGGCCCC
AATGGCCGAAGAGTACCCCATGTACAGTGGAGAGAAAGCTACATTACAGGCGCTCAAGGA
GAAGTTTCCACAGGAGGAAGCTATCATTGACAAGTATATAAAGCTGGTTAAGGTGGTATCCA
GTGGAGCCCCCTCATGCCATCCTGTTGAATTCCTCCATTGCCGTGGTTCAGCTCCTCGAC
AGGTGTGGGCTGTGACTCGTTTTCTCTCCATTCTTCAAGCATCCACCCAGAGCCTGGCTGA
GGTCTGCAGCAGCTGGGGGCTCCTCTGAGCTCCAGGCAGTACTCAGCTACATCTTCCCCA
CTTACGGTGTCAACCCCAACACAGTGCCTTTTCCATGCACGCCCTGTGGTCAACCACTAC
ATGAAAGGAGGCTTTTTATCCCCGAGGGGTTCCAGTGAAATTTGCCTTCCACACCATCCCTGT
GATTACGCGGGCTGGGGGCGCTGTCTCACAAGGGCACTGTGCAGAGTGTGTGTCTGGACT
CAGCTGGGAAAGCTGTGGTGTCAAGTGTGAAGAAGGGGCATGAGCTGGTGAACATCTATTGC
CCCATCGTGTCTCCAACGCGAGGACTGTTCAACACCTATGAACACCTACTGCCGGGGAACGC
CGCGTCTGCCAGCTGTGAAGCAGCAACTGGGGACGGTGCAGGCGGCTTAGGCATGACCT
CTGTTTTCTATCTGCTGCGAGGCACCAAGGAAGACCTGCATCTGCCCTCCACCACTACTAT
AGGACCGATTCCAGAGCCCGGTCCACCATGATCATGCTCATACCCACTGCCACGAGTGGTTT
GAGGAGTGGCAGGCGGAGCTGAAGGGAAGCGGGGCGAGTACTGAGACCTTTCAAAAATCTC
CTTTGTGGAAGCCTCTATGTCAAGTGGTCTGAAACTGTTCACCACTGGAGGGGGAAGGTTG
AGAGTGTGACTGCAGGATCCCCACTCACCAACAGTTCATCTGTGGCTGTCCCCGAGGTGCC
TGCTACGGGGCTGACCATGACCTGGGCGGCTGCACCCCTTGTGTATGGCCCTCTTAGGGC
CCAGAGCCCCATCCCCAACCTCTATCTGACAGGCCAGGATATCTTACCTGTGGATGGTTCG
GGGCGCTGCAAGGTGCCCTGCTGTGCAGCAGCGCCATCTTGAAGCGGAACCTGTACTCAGC
CTTAAGAATCTTGATTCTAGGATCCGGGCACAGAAGAAAAAGAA**TAG**TTCCATCAGGGAGG
AGTCAGAGGAATTTGCCAATGGCTGGGGCATCTCCCTTGACTTACCCATAATGTCTTTCTG
CATTAGTTCTTGACGATATAAAGCACTCTAATTTGGTCTGATGCCTGAAGAGAGGCCTAG
TTTTAATCACAATTCGAATCTGGGGCAATGGGAATCACTGCTTCCAGCTGGGGCAGGTGAGA
TCTTTACGCCCTTTATAACATGCCATCCCTACTAATAGGATATTGACTTGGATAGCTTGATG
TCTCATGACGAGCGGCGATGTCATCCCTACCCATGCCTCCTAATCTCAGTGATCAAGCGGA
ATATTCCATCTGTGGATAGAACCCCTGGCAGTGTGTGCTCAGCTCAACCTGGTGGGTTCAGTTC
TGTCTTGAGGCTTCTGCTCTCATTCATTAGTTAGTGCTACGCTGCACAGTTCTACACTGTCAAGG
GAAAAGGGAGACTAATAGGGCTTAACCTAAAACCTGGGCGTGGTTTGGTTGCCATTCCTATA
GGTTTGGAGGCTCTAGATCTCTTTTGTGCTGGGTTCTAGTGGCTCTCAGGGGACAGGAAT
GGCTGTGCTGTGGCCAGTGTGGTCTGGAGCTTTGGGCTAACAGCAGGATCCATCAGTTAGTA
GGTGCGATGTCAGATGATCATATCCAATTCATATGGAAAGTCCCCGGCTGTGCTTCTCTTATCA
TCGGGGTGGCAGCTGGTTCTCAATGTGCCAGCAGGGACTCAGTACCTGAGCCCTCAATCAAGC
CTTATCCACCAATAACAGGGAAGGGGTGATGCAGGGAAGGGTGACATCAGGAGTCAGGGA
TGGACTGGTAAAGTGAATACCTTTGCTGGGCTGAAGCAGGCTGCAGGGCATTCCAGCCAAGGG
CACAGCAGGGGACAGTGCAGGGAGGTGTGGGGTGAAGGAGGGAAGTCAATCAGAAAAGGA
AAGCCACGGAATGTGTGTGAAGCCCAAGAAATGGCAATTTGCAGTTAATAGCAGATGTGGGG
TTAGACAGGTAGGTGATGCAAGCTCAAGGTTTGGAAAAATGACTTTTCAGTTATGCTTTG
GTATCAGACATACGAAAGGCTCTCTTTGATGTTCTGTTAATGTAACATTAATAAATTTATG
ATTCCATTGCTTTAAAAA

FIGURE 64

MWLPLVLLLA VLLLA VLCKVYLGLFSGSSPNPFSE DVKRPAPLVTDKEARKKVLKQAFSAN
QVPEKLDVVVIGSGFGGLAAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNGLEFDTGIHYIG
RMEEGSIGRFILDQITEGQLDWAPLSSPFDIMVLEGPNRKEYPMYSGEKAYIQGLKEKFPQ
EEAIIDKYIKLVKVSSGAPHAILLKFLPLPVVQLLDRCGLLTRFSPFLQASTQSLAEVLQQ
LGASSELQAVLSYIFPTYGVTPNHSAFSMHALLVNHYMKGGFYPRGGSSEIAFHTIPV IQRA
GGAVLT KATVQSVLLDSAGKACGVS VKKGHEL VNIYCP IVVSNAGLFNTYEHLLPGNARCLP
GVKQQLGTVRPGLGMTSVFICLRGT KEDLHLPSTNYYVYYDTMDMQAMERYVSMPREAAEH
IPLFFAFPSAKDPTWEDRFPGRSTMIMLIPTAYEWFEEWQ AELKGKRGSDYETFKNSFVEA
SMSVVLKLPQLEGKVESVTAGSPLTNQFYLAAPRGACYGADHDLGR LHPCVMASLRAQSPI
PNLYLTGQDIFTCGLVGALQGALLCSSAILKRNLYSDLKNLDSRIRAQKKKN

[illegible]

FIGURE 66

MRVRIGLTLLLCAVLLSLASASSDEEGSQDESLSKTTLTSDSVKDHTTAGRVVAGQIFLD
SESELESSIQEEEDSLKSQEGESVTEDISFLESPNPENKDYEEPKVRKPALTAIEGTAHG
EPCHFPPFLDKEYDECTSDGREDDGRLWCATTYDYKADEKWGFCETEEEEAAKRRQMQEAEEM
YQTGMKILNGSNKKSQKREAYRYLQKAASMNHTKALERVSYALLFGDYL PQNIQAAREMFEK
LTEEGSPKGQTALGFLYASGLGVNSSQAKALVYYTFGALGGNLIAHMLVLSRL

FIGURE 67

CTTCCCAGCCCTGTGCCCCAAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCCT
GCCTCCCTGCCTCTGGCCATGGCCTGCCGGTGCCTCAGCTTCTTCTGATGGGGACCTTCCT
GTCAGTTTCCCAGACAGTCTTGGCCCAGCTGGATGCACTGCTGGTCTTCCCAGGCCAAGTGG
CTCAACTCTCCTGCACGCTCAGCCCCAGCACGTCACCATCAGGGACTACGGTGTGTCTGG
TACCAGCAGCGGGCAGGCAGTGGCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCA
CCACCGGCCTGTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCCACAAATGCCT
GTGTCTCACCATTAGTCCCGTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGC
TACGGCTTTAGTCCCTAGGGGTGGGGTGTGAGATGGGTGCCTCCCCTCTGCCTCCCATTCT
GCCCCTGACCTTGGGTCCCTTTTAAACTTTCTCTGAGCCTTGCTTCCCCTCTGTAAATGGG
TTAATAATATTCAACATGTCAACAAC

CGGCTTTAGTCCC

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MACRCLSFLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAG
SAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVPQEDDADYYCSVGYGFSF

FIGURE 69

GCGCGCCCGCCCCGAGACCGGGGCCCGGGGCGCGGGGCGCGGGGATGCGCGCCCGGGGCGCG
 CGATGACCGCGGAGCGCAGCCGCGCGGGCCCGGCCCTGACCCCGCGCCCGCCCGCTGAGCCCC
 CCCGCGGAGGTCCGGACAGGCCGAGATGACGCCGAGCCCCCTGTTGCTGCTCTCTGCTGCGCG
 CCGCTGCTGCTGGGGGCCCTTCCACCAGCGCCGCCGCGCGCCGAGGCCCCCAAAGATGGCGGAC
 AAGGTGGTCCACCGCAGGTGGCCGGCTGGGCGGCACCTGTGCGGCTGCAGTGGCCAGTGGGA
 GGGGAGCCCGCGCGCTGACCATGTGGACCAAGGATGGCCGACCATCCACAGCGCGTGGGA
 CGCGCTTCCGCGTGTCTGCGCGAGGGGTGAAGGTGAAGCAGGTGAGCGGGAGGATGCCGGC
 GTGTACGTGTGCAAGGCCACCAACGGCTTCGGCAGCCTGAGCGTCAACTACACCCCTCGTCTGT
 ACTGGATGCATTAGCCACGAGGAGGAGAGCCTGGGGCCCGACAGCTCTCTGGGGGTCAAG
 AGGACCCCGCCAGCCAGCAGTGGGCACGACCGCGCTTCACACAGCCCTCCAAAGATGAGGCGC
 CGGCTGATCGCAGCGGCCGTGGGTAGCTCCGTGCGGCTCAAGTGCGTGGCCAGCGGGCACCC
 TCGGCCCGACATCAGCTGGATGAAGGACGACAGGCCCTTGACGCGCCAGAGGCCGCTGAGC
 CCAGGAAGAAGTGGACACTGAGCCTGAAGAACCTGCGGCCGGAGGACAGCGGCAATAC
 ACTGCGCGCGTGTGAAACCGCGCGGGCGCCATCAACGCCACCTACAAAGTGGATGTGATCCA
 GCGGACCCGTTCCAAAGCCGCTGTCTACAGGCACGACCCCGTGAACACGACGGTGGACTTCG
 GGGGACCAAGCTCTTCCAGTGCAGAGTGGCAGCGAGCTGAAGCCGGTGTATCCAGTGGCTG
 AAGCGCTGGAGTACGGGCCCGGAGGGCCGCCACAACTCCACCATGCATGTGGGCGGCCAGAA
 GTTTTGTGTGCTGCCACCGGGTGACGTGTGGTTCGGGCCCGGACGGCTCTTACCTCAATAAGC
 TGCTATGACCCGTTGCCCGCAGGACGATGCGGGCATGTACATCTGTGCCGTCACACCAACC
 ATGGGCTACAGCTTCCGACAGCGCTTCTTCCACCGTGTGCGCAGACCCAAACCGCCAGGGCC
 ATGCTGGCCCTCTCTGCTCTCGGCCACTAGCTGCCGTGGCCCGTGGTCATCGCATGCCATCCAG
 CCGCGCTGTCTTATCTTGGGCACCCCTGCTCTGTGGCTTTGCCAGGCCAGGAAGACCG
 TGACACCCCGCCCTGCCCTCCCTGCTGGCGACCGCCCGCGGGGACGGCCAGCGCCAGC
 CAGCGGAGACAGGACCTTCCCTCGTTGGCGCCCTCAGCGCTGGCCCTGGTGTGGGGCTGT
 GTGAGGAGATGGGTCTTCGGCAGCCCCCAGCACTTACTGGCCCGAGGCCAGTTGCTGGC
 CCTAAGTTGTATCCCAAACTCTACACAGACATCCACACACACACACACACACTCTCACAC
 ACACCTCACAGTGGAGGCAAGGTCCACAGCAGATCCACTATCAGTGCCTAGACGGCACCCGT
 ATCTGCAGTGGGCACGGGGGGGGCCGCCAGCAGGCAGACTGGGAGGATGGAGGACGGAGCT
 GCAGACGAAGGCAGGGGACCCATGGCGAGGAGGAATGGCCAGCACCCAGGCAGTCTGTGTG
 TGAGGCATAGCCCCCTGGACACACACACAGACACACACACTACCTGGATGCAATGTATGCAC
 ACACATGCGCGCACACGCTGCTCCCTGAAGGCACACGTCACGCACACGCACATGCACAGATATG
 CCGCTCTGGGCACACAGATAAGCTGCCAAATGACGCGCACACGCACAGAGACATGCCAGAACA
 TACAAGGCATGCTGCTGAACATAACACACGCACACCCATGCGCAGATGTGCTGCTGGACA
 CACACACACACAGGATATGCTGTCTGGACGCACACAGTGCAGATATGGTATCCGGACACA
 CAGTGCACAGATATGCTGCTGGACACACAGATAATGCTGCTGCACACACATGCACCG
 ATATTGCTGGACACACACACACACACCGCTGCACAGATATGCTGCTGGACACGCACAC
 ACATGCAGATATGCTGCTGCACACACACTTCACAGACACAGTGCACAGCGCAGATATGCT
 GCCTGGACACACGCAGATATGCTGTCTAGTCACACACACACGCAGACATGCTGTCCCGGACAC
 ACACACGCATGCACAGATATGCTGTGCGGACACACACGCACAGATATGCTGCTGGAC
 ACACACACAGATAATGCTGCTCAACACTCACACACGTCAGATATGCTGCTGGACACACACA
 TGTGCACAGATATGCTGTGGACATGCACACGTCAGATATGCTGCTGGGACACACACG
 CAGGCACACATGCAGATATGCTGCTGGGACACACTTCCGACACACATGCACACACAGGT
 GCAGATATGCTGCTGGACACACACACAGATAATGCTGCTCAACACTCACACACGTCAGAGA
 TATTGCTGGACACACACATGTGCACAGATATGCTGCTGGACATGCACACACGTCAGACATA
 TGCTGTGCGGATACACACGCACACACATGCAGATATGCTGCTGGGACACACTTCCGGA
 CACACATGCACACACAGGTGCAGATATGCTGCTGGACACACGAGACTGACGTGCTTTGG
 GAGGTTGTGCGGTGAGGCTGCAGTACGTGTGCGGTGAGGCTCATAGTGTATGAGGGACTTT
 CCCTGCTCCACGCTCACTCCCCAACTCTGCCCGCTCTGTCCCGCTCAGTCCCCCGCTTGG
 CATCCCGCTGTGCTGCTGCTGCTGCTGGCGCTATTTTTGCCACTGCTTGGGTGGCCACG
 AGTCCCCCTACTGCTGTGGGCTGGGTTGGGGGACAGCAGCCCCAGCCCTGAGAGGCTGGAG
 CCGATGGCTAGTGGCTCATCCCCAGTGCAATCTCCCCCTGCACAGAGAAGGGGCTGGTA
 TTTATATTTAAGAAATGAAGATAATATTAATAATGATGGAAGGAAGACTGGGTGTGAGGAGC
 TGTGCTCTCTCTGGGGCCCGGACCCCGCTGGTCTTTCAGGATGCTGATGACCCACCCCC
 GTCCAGGCCAGACACACCCCCCACCCTGCTGCTGCTGGGCCCCAGATCTCTGTAAATTTTA
 TGTAGAGTTTGGAGCTGAAGCCCCGTATATTTAATTTATTTTGTAAACACAAA

104117.11406660

MTTSPSLLLLLLPPLLGAFFPAAAARGPPKMAKDVVPRQVARLGRTVRLQCFVEGDPPPLTM
WTKDGRTIHSGWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGSLSVNYTLVLLDDISPGK
ESLGPDSSSGGQEDPASQQWARPRFTQPSKMRVRVIARVPGSSVRLKCVASGHPRPDITWMK
DDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQRTRSKPV
TGTHPVNTTVDFGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGRHNSTIDVGGQKFFVLLPTGD
VWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLTVPDPKPPGPPVASSSSA
TSLPWPVVIGIPAGAVFILGTLTLLWLCQAQKKPCTPAPAPPLPGHRPPGTARDRSGDKDLPS
LAALSAGPGVGLCEEHGSAPAPQHLLGPGPVAGPKLYPKLYTDIHTHTHTSHTHSHVEGKV
HOHIHYOC

[illegible]

FIGURE 72

MVGTKAWVFSFLVLEVTSVLGRQTMLTQSVRRVQPGKKNPSIFAKPADTLES PGEWTTWFNI
 DYPGGKGDYERLDAIRFYYGDRVCARPLRLEARTTDWT PAGSTGQVVHGS PREGFWCLNREQ
 RFGQNC SNYTVRFLCPPGSLRRDTERIWS PWS PWSKCSAACGQTGVQTRTRICLAEMVSLCS
 EASEEGQHCMGQDCTACDLT CPMGQVNADCDACMCQDFMLHGAVSLPGGAPASGAAYLLTK
 TPKLLTQTDS DGRFRIPGLCPDGKSILKITKVKFAPIVL TMPKTS LKAATIKAEFVRAETPY
 MVMNPETKARRAGQSVSLCCKATGKPRPDKYFWYHNDTL LDPSLYKHESKLVLRLKQHQAG
 EYFCKAQSDAGAVKSKVAQLIVTASDETPCNPVPESYLIRLPHDCFQ NATNSFYDVGRCPV
 KTCAGQQDNGIRCRDAVQNCCGISKTEEREIQCSGYTLPTKVAKECSCQRC TETR SI VGRV
 SAADNGEPMRFGHVYMGNSRVSM TGYKGTFTLHVPQDTERLVLT FVDRLQKFVNTTKVLPFN
 KKGS AVFHEIKMLRKEPIT LEAMETNII PLGEVVGEDPMAELEIPSR SFYRQNGEPEYIGKV
 KASVTFLDPRNISTATAAQTDLNF INDEGDTFPLRTYGMFSVD FRDEVTSEPLNAGKV KVLH
 DSTQVKMPEHISTVKLWSLNPDTGLWEEEGDFKFENQRRNKREDRTFLVGNLEIRERRLFNL
 DVPESRRCFVKVRAYRSE RFLPSEQIGVVISVINLEPRTGFLSNPRAWGRFDSVITGPNGA
 CVPAFCDDQSPDAYSAYVLASLAGEELQAVESSPKFNPNAIGVPPYLNKLNRYRRTDHEDPR
 VKKTAFAQISM AKPRPNSAEESNGPIYAFENLRACEEAPPSAAHFRFYQIEGDRYDNTVPFN
 EDDPMSWTE DYLAWWPKPMEFRACYIKVKIVGPLEVNVRSRNMGGTHRRTVGKLYGIRDVRS
 TRDRDQPNVSAACLEFKCSGMLYDQDRVDRTL VKVIPQGSRRASVNPMLHEYLVNHLPLAV
 NNDS EYTM LAPLDPLGHNYGIYTVTDQDPRTAKEIALGRCFDGTSDGSSRIMKSNVGVALT
 FNCVERQVGRQSAFYQLQSTPAQSPAAGTVQGRVPSRRQQRASRGQRQGGVVASLRFPRVA
 QQPLIN

FIGURE 73

CTGCAAGTTGTTAAACGCCATAACACACAAGTATGTTAGGCTTCCACCAAAGTCCTCAATATACCTGAATACGCAC
 AATATCTTAACTCTTCATATTTGGTTTTGGGATCTGCTTTGAGGTCCCATCTTCATTTAAAAAAAATACAGAG
 CCTACCTACCCGTACGCATACATACATATGTTATATATATGTAACCTAGACAAAGATCGCAGATCATAAAGC
 AAGCTCTGCTTTAGTTTCCAAGAAGATTACAAGAATTTAGAGATGTTATTTGCAAGATCCCTGCGATTCTATG
 CCCTTTGGGTTTACGGTCTCTCAGTGATGATGAGCCCTACCCTTTGGTTTGGGGACATTATGATTTGTGAAGAT
 CAGATTTACACGGAGAAAGGAAAGTTGGGATTACATGGCCTGCCAGCCGGAATCCAGGCATGACAAATA
 TCTGAAGTGAACCTCGATCCTCCGGATATTACCTTGGAGACCCTCTGAGACGTTCTGTGCAATGGGCAATTC
 CCTACATGTGCAATATAGTGATGTGATGCGAGTACCCTGAGCTGGCACACCCCCCTGAGCTGATGTTGATTTT
 GAAGGAAGACATCCCTCCACATTTTGGCAGTCTGCCACTTGGGAAGGATATCCCAAGCCTCTCCAGGTTAACAT
 CACTCTGTCTTGGAGCAAAACATTGAGCTAACAGACAACTAGTTATTACCTTTGAATCTGGGCGTCCAGACC
 AAATGATCTCGGAGAGTCTCTCGATTATGGACGAACATGGCAGCCCTATCAGTATTATGCCACAGACTGTTA
 GATGCTTTTACATGGATCCTAAATCCGTGAAGGATTATCACAGCATACGGTCTTGAATCATTTTGACAGA
 AGAGTACTCAACAGGGTATACAACAAATAGCAAAATATCCACTTTGAATCAAAGACAGGTTCCGCGTTTTTG
 CTGGACCTCGCCTACGCAATATGGCTTCCCTCTACGGACAGCTGGATACAAAGAACTCAGAGATTCTTTT
 ACAGTCACAGACTGAGGATAAGGCTGTTAAGACCAGCCGTTGGGGAAATATTTTATGATGAGCTACACTTTGGC
 ACGCTACTTTTACGCGATCTCAGACATAAAGGTGCGAGGAAGTGCAAGTGTAACTCTCATGCCACTGTATGTG
 TGTATGACACAGCAAAATGACATGCGAATGTGAGCACAACACTACAGTCCAGACTGTGGGAATGCAAGAAG
 AATTATCAGGGCCGACCTTGGAGTCCAGGCTCCTATCTCCCCATCCCAAAGGCACTGCAAAATACCTGTATCCC
 CAGTATTTCCAGTATTTGGTACGAATGTCTGCGACACAGAGCTCTGCACTGCCAGAACGAGGAGACGTGCCACA
 ACAACGTGCGCTGCTTGCCCGGCCGATACACGGGCATCTCTGCGAGAAGCTGCGGTGCGAGGAGGCTGCCA
 AGCTGCGGCTCCGACTCTGGCCAGGGCGCGCCCCGCGACGCGACCCGACGCTGCTGCTGCTGACCCGCTGCT
 GGGAAACGCGCAGCCCCCTGTTGTTCTAGGTGTCACTCCAGCCACACCGGAGCGGCTGTGCGTGGGGGAAGCA
 GACACAACCCAAACATTTGCTACTAACATAGGAAACACACATACAGACACCCCCCTCAGACAGTGTACAAA
 CTAAGAAGGCTTAAGTGAACATAGCCATATTTATCACCGTGGACAGCAGTCCGAGTGAACAGTGTAAATTC
 TGACTCCAGAGGAGTTGGCAGCTGTTGATATTACTGCAAAATCAGTTGCCAGCTGCGAGCATATTTGGGA
 TTGGAAAGGCTGCGACAGCCCCCAACAGGAAGAGCAAAAAACAACAAATCAACCGACTTAAACACATTGGC
 TACTCTAGCGTGGTGGCCCTAGTACGACTCCGCCAGTGTGTGGACCAACAAATAGCATTTCTTGCTGTGAG
 GTGCAATTGTGGGATAAGGAATCTGTTACAAAGCTGCATATTGGCCTGCTTCCGTCCCTGAATCCCTTCCAAC
 CTGTGCTTTAGTGAACGTTGCTCTGTAACCCCTGTTGGTTGAAGAGTTCTTTGTCTGATGTTAGTGATGCACA
 TGTGTAAACGCCCCCTCTAAAAGCGCAAGCCAGTCATAACCCCTGTATATCTTAGCAGCACTGAGTCCAGTGGCA
 GCACACCCCACTATACAAAGAGTGGCTATAGGAAAAAGAAAGTGTATCTATCTCTTTGTATTCAATGAAGTT
 ATTTTCTCTGAACTACTGTAATATGTAGATTTTGTATTATTGCCAATTTGTGTACAGACAATCTGTTAAT
 GTATCTAATTCGAATCAGCAAGAGCTGACATTTTATTGTCTCTTTCGTCTGTTTGTGTTCACTGTGCAGA
 GATTTCTCTGTGAAGGCAAGCAAGCTGCTGGCATCAAAGAATATCAGTTTACATATATAACAAGTGAATAAGA
 TTCCACAAGAGCAATCTTAAATGTTTCTGTGTGCTTTAACACTGGGAAGATTAAAGATAAAAACTCCTGCA
 TAAACGATTTTTCAGGATTTGTATTGCAATTTCTTAAGATGAAAGGAACAGCCACCAAGCAGTTTCACTCACT
 TTACTGATTTCTGTGTGAGCTGAGTACATTGAGCTGACGAATTTAGTCCAGGAAGATGGATTGATGTTCACT
 AGCTTGGACAACCTCTGCAAAATATGAGACTATTTCCACTTGGGAAAAATACACAGCAAAAAAAAAAAAAA
 AAAAAA

MYLSRSLSIHALWTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLK
VKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELAHPPELMFDFEGRHPSTFWQSATWK
EYPKPLQVNITLSWSKTIELTDNIVITFESGRPDQMLEKSLDYGRTWQPYQYYATDCLDAF
HMDPKSVKDL SQHTVLEIICTEESTGYTTNSKIIHFEIKDRFALFAGPRLRNMASLYGQLD
TTKKLRDFFVTDLRIRLLRPVAGEIFVDELHLARYFYAISDIKVRGRCKCNLHATVCVYDN
SKLTCECEHNTTGPDCGCKCKNYQGRPWSPGSYLP PKGTANTCIPSISSIGTNVCDNELH
CQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSCGSDSGQGAPPHGTPALLLLTTLGTAS
PLVF

CCACGCGTCCGGGTGACCTGGGCCGAGCCCTCCCGGTCCGCTAAGATTGCTGAGGAGCGG
CGGGTAGCTGGCAGGCCCGACTTCCGAAGCGCCGCTCCGGGCGAGGTGTCCTCATGACTT
CTCTTGTGGACCA**ATG**TCCGTGATCTTTTTTGCTGCGTGGTACGGGAAGGGATGGACTGCC
CCTCTCAGCCTCTACTGATTTTTACCACACCCAAAGATTTTTTGAATGGAGGAGACGGCTCA
AGAGTTTAGCCTTGCAGCTGGCCAGTATCCAGGTGAGGTTCTGCAGAAGGTTGTACTT
AGTATACATTTTTCTTCTTCGGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTCC
AGCAGCCATGGCCTTCTGCTTCTCGGAGACCCTGTGGTGGGAATTCACAGCTTCTATGACA
CTACCTGCATTGGCCTAGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTAG
AAAGTGAAGTGGCATTTTAACTATGTAAGTTCCTCTCAGATGGAGTGCAGCTTGGAAAAAT
TCAGGAGGAGCTCAAGTTGCAGCCTCCAGCGTTTCTACTCTGGAGGACACAGATGTGGCAA
ATGGGGTGATGAATGGTCACACACCATGCACTTGGAGCCTGCTCCTAATTTCCGAATGGAA
CCAGTGACAGCCCTGGGTATCTCTCCCTCATTCTCAACATCATGTGTGCTGCCCTGAATCT
CATTGAGGAGTTTCACTTGCAGAACATTCTTTCAGGATCCAAGGAGCTGGTTCTGCTGGT
TGGACCAAACCTCGT**TGA**GCCAGCCACCCCTGACCCAAATGAGGAGAGCTCTGATTCTCCCAT
CCGGGAGCAGTGATGTCAAACCTTCTGCTGCTGGGGAATCTCATCAGCAGGAGCCTGTGGA
AAAGGGCATGTGAGTGAAATCTGGGAATGGCTGGATTCCGAAACATCTGCCCATGTGTATTG
ATGGCAGAGCTGTGCCCCACAAGCGCCTTTTATTAGGGTAAATAAACAAATCCATTCTAT
TCCTCTGACCCATGCTTAGTACATATGACCTTTAACCCCTACATTTATATGATTCTGGGGT
GCTTCAGAAGTGTTATTTTCATGAATCATTTCATATGATTTGATCCCCAGGATCTATTTTGT
TTAATGGGCTTTTCTACTAAAAGCATAAAATACTGAGGCTGATTAGTCAGGCAAAACCAT
TTACTTTACATATTCGTTTTCAATACTTGCTGTTTCATGTTACACAAGCTTCTTACGGTTTTT
TTGTAACAATAAAATTTTGAGTAATAATGGGTACATTTTAACAACTCAGTAGTACAAC
TAAACTTGATATAAAAGTGTGTAAAAATGTATAGCCATTTATATCCTATGTATAAATTAATG
AGGTGGCTTCAGAAATGGCAGAATAAATCTAAAGTGTTTATTAATAAAAAAAAAAAAAAAAAA
AAAAG

MSVIFFAFCVVRVRDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPRGRSAEGCDFSIHF
SSFGDVACMAICSCQCPAAMAFCFLETLWWEFTASYDTTCIGLASRPYAFLEFDSIIQKVVK
HFNYVSSSQMECSLEKIQEELKLQPPAVLTLEDTDVANGVMNGHTPMHLEPAPNFRMEPVTA
LGILSLILNIMCAALNLRGVHLAEHSLQDPRSWFCWLDQTS

FIGURE 77

TGCTTCCTGGAGACCCTGTGGTGGGAATTCACAGCTTCNTATGACACTACCTGCATTGGCNT
AGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTCAGAAAGTGAAGTGGCATT
TTAACTATGTAAGTTCCTNTCAGATGGAGTGCAGCTTGGAAAAAATTCAGGAGGAGCTCAAG
TTGCAGCCTCCAGCGGTTCTCANTATGGAGGACACAGATGTGGCAAATGGGGT

CTCAGCGCGCGCTTCTCTCGTAGCGAGCCTAGTGCGCGGGTGTTCGATTGAAACGTGAGCGCGA
CCCGACCTTTAAAGAGCTGGGGAGCAAAAGGGAGGACAGAGCCCTTTAAACAGAGGCGGGTGGTG
CCTGCCCTTTTAAAGGCGGGGCGTCCGGACAGCTGTATCTGAGCCCCAGACTGCCCCGAGTT
TCTGTGCGAGGCTGCGAGGAAAGGCCCTAGGCTAGGCTGTGGGTGCTTGGCGGCGCGGCTT
CCTCCCGGCTGCTCTCCCGGGGCCAGAGGCTCCGCTTCAGTCACTGCTGAGCAGAGTA
TGGAAGCACTGACTACGAAGTGCTATCCGTGCGAGAACAGTATTTCCAGCAGAGGATCCGC
GAGTGATTATTATCAACACTTCTGTTTGCACACTGTATACCTCTGCCACACTCTCTCTGAG
CCGCTTCAAGAAGCGCTTCTGAGTTTACCACAGCTGGATGATGAAGATGCCACCTTCAACAGA
TTGGCTGCTGAGCTGTGACACTTTACCTTGGCAATTGCCTGGGTGCTGTCTGTCTCTTGGCC
TTCTCCATCATCAGCAATGAGGTGCTGCTCTCTCTCGCTCCGAACACTACTACATCCAGTGGCT
CAACGGCTCCCTCATCATGAGCTGGCTTGGAACTTGTTTTCTCTCCCAACCTTCTCCCTCA
TCTTCTCATGCCCTTTGCATATTCTTCTACTGAGTCTGAGGGCTTTGCTGGCTCCGAAAG
GGTGCTCTGGGCGGGGTCTATGAGACAGTGGGTGATGTGTGATGCTCTCACTCTGCTGGTGCT
AGGTATGTGTGGTGGCATCAGCACTGTGGACAAGAACAGGCCAACAGAGAGTACTCT
ATGACTTTTGGGAGTACTATCTCCCTACTCTTACTCATGATCTCTCTTCTTGGGGTGTCT
CTGCTCTGGTGTGATCACTCCACTGGGTCTCGCCCGCATGTTCTCCGTCACCTGGGAAGTGTCT
AGTCAAGCCCGCGTCTGCTGGAAGACTGGAGGACAGGCTGACTGCTCAGCCTTTGAGGAGG
CAGCCCTGAGCCGAGGATCTGTAATCTACTTCTCTGGTGCCTTTAGACATGGAGCTG
TTCACACACAGGTCCTGGCTCTGCAGACACAGAGGGTCTGCTGTGGAGAAGCGGCGAAGGG
TTCAGCCTGGCAACGGAACCTGGGCTACCCCTGGCTATGCTGTGCTTGTGCTGCTGACGG
GCCTTCTGTGCTCACTTGTGGCCATCCACATCTCGTGAGGCTGCTCATGATGAGGCTGCCAT
CCCGAGGACTGCGAGGTACCTCTTATGGCCAGGTCTCCTCTCCAAGCTGGGCTCTTTGG
TGCCGTCATTAGGTTGTACTCATCTTTTACCTAATGGTGTCTCACTGATGTGGGCTTCTATA
GCTCTCCACTCTCTCCGAGAGTCTCGGCGCCAGATGGCACAGCACTGCCATGCGCAGATAAAT
GGAACTGTGTCTGTCTCTGTGCTTAAGCTCAGCACTTCTGTCTTCTCTCGAACCCTGGG
GCTCACTCGCTTTGACCTGCTGGGTGACTTGTGGACGCTTCAACTGGCTGGGCAATTTTCTAC
TTGTGTTTCTCTACAACGCAAGCTTTGACGCGCTCACCACACTGCTGTGTGTGAAGACTTC
ACTGCAGCTGTGCGGGCAGAGCTGATCCGGGCCCTTGGGCTGGACAGACTGCCGTGCGCCCT
CTCCGGTTCCTCCCGAGGATCTAGGAAGAACCCAGCACCA**GGAGCT**CCAGCTGGGGTGGGA
AGGAAAAAATCGACACTGCCATCTGCTGCTAGGCGCTGGAGGAAGCCCAAGGCTACTTGG
ACCTCAGGAGCTGGAATCTGAGAGGTTGGGTGGCAGAGGGGAGCAGGCCATCTGCATATT
GCATAATCTGAGCCAGAGTTTGGGACCAAGCACTCTGCTTTTCTCACTATTAACTGTGGCT
CAGCATGGGGTAGGGCTGGGTGACTGGGTCTAGCCCTGATCCCAAATCTGTTTACACATCA
ATCTGCTCACTGCTGTTCTGGGCCATCCCCATAGCCATGTTTACATGATTTAGTGTGCAAT
AGGGTGGGTAGGGGCAAGGAAGGACTGGCCAGGGCAGGCTCGGAGATAGATGTCTTCC
CTTGCTCTGGGCCAGAGGCTAAGCACTGTGCTATCTGGAGGGGCTTTGGACCACCTG
AAAAACCAAGGGATAGGGAGGAGGAGGCTTCAGCCATCAGCAATAAAGTTGATCCCGAGGA
AAAAAA

MEAPDYEVLSVREQLFHERIRECIISTLLFATLYILCHIFLTRFKKPAEFTTVDDEDATVVK
IALELCTFTLAIALGAVLLLPFSIISNEVLLSLPRNYIQWLNGLIHGLWNLVFLPNLSL
IFLMPFAYFTESEGFAGSRKGVLG RVYETVVMMLLTLLVLGMVWVASAIVDKNKANRESL
YDFWEYYPYLYSCISFLGVLLLLVCTPLGLARMSVTGKLLVKPRILLEDLEEQLYCSAFEE
AALTRRICNPTSCWLPDMELHRQVLAQTQRVILLEKRRKASAWQRNLGYPLAMLCLLVLT
GLSVLIVAIHILELLIDEAAPRGMQGTSLGQVSFSKLSFGAVIQVVLIFLYLMVSSVVGFY
SSPLFRSLRPWHDAMTQIIIGNCVLLVLSSALPVFSRTLGLTRFDLLGDGFRNWLGNFY
IVFLYNAAFAGLTTLCLVKTFTAAVRAELIRAFGLDRPLPVSFGFPQASRKTQHQ

GGCTGCGCAGGGAAGGCCCTTGGGTTGGTCTTGGTTGCTTGGCGGCGCGGNTTCNTCCCC
GCTCGTCTCCCGGGCCAGAGGCACCTCGGCTTCAGTCACTGCTGAGCAGAGTATGGAAGC
ACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCATATTCGCCAGAGGATCCGCGAGTGTA
TTATATCAACACTTGTGTTTGCAACACTGTACATCTCTGCCACATCTTCTGACCCGCTTC
AAGAGCCTGCTGAGTTACACACAGCTGGATGATGAAGATGCCACCG

FIGURE 81

GACCGACCTTAAGAGTGGGAGCAAAGGGAGGACAGAGCCTTTTAAACGAGGCGGTGGTGC
CTGCCCTTTAAGGGCGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCGAGTTTC
TGTCGCAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGTGCTTGGCGGCGGCGGCTTCCT
CCCCGTGTNTCCCGGGCCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGA
AGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGT
GTATTATATCAACACTTCTGTTTGCAACACTGTACATCNTCTGCCACATCTTCCTGACCCGC
TTCAAGAAGCCTGCTGAGTTCACCACAGTGATGATGAAGATGCCACCGTCAACAAGATTGC
GCTCGAGCTGTGCACCTTTACCCCTGGCAATTGCCCTGGGTGCTGTCTGCTCCTGCCCTTCT
CCATCATCAGCAATGAGGTGCTGCACTCCC

FIGURE 82

GATGTGCTCCTTGGAGCTGGTGTGCAGTGTCTGACTGTAAGATCAAGTCCAAACCTGTTTT
GGAATTGAGGAACTTCTCTTTTGATCTCAGCCCTTGGTGGTCCAGGTCTT**CATG**CTGCTGT
GGGTGATATTACTGGTCCTGGCTCCTGTGCAGTGGACAGTTTGCAAGGACACCAGGCCATT
ATTTTCCTCCAGCCTCCATGGACCACAGTCTTCCAAGGAGAGAGAGTGACCCTCACTTGCAA
GGGATTTTCGCTTCTACTCACCACAGAAAAAATAATGGTACCATCGGTACCTTGGGAAAGAAA
TACTAAGAGAAACCCAGACAATATCCTTGAGGTTCAGGAATCTGGAGAGTACAGATGCCAG
GCCCAGGGCTCCCCTCTCAGTAGCCCTGTGCACCTTGGATTTTCTTCAGAGATGGGATTTCC
TCATGCTGCCCAGGCTAATGTTGAACTCCTGGGCTCAAGTGATCTGCTCACCT**TAG**GCCTCTC
AAAGCGCTGGGATTACAGCTTCGCTGATCCTGCAAGCTCCACTTTCTGTGTTTGAAGGAGAC
TCTGTGGTTCTGAGGTGCCGGCAAAGCGGAAGTAACACTGAATAATACTATTTACAAGAA
TGATAATGTCCTGGCATTCCTTAATAAAAGAACTGACTTCCAAAAAAAAAAAAAAAAAAAAA
AAA

83/330

FIGURE 83

MLLWVILLVLAPVSGQFARTPRPIIFLQPPWTTVFQGERVILTCKGFRFYSPQKTKWYHRYL
GKEILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDIFSSEMGFPHAAQANVELLGSSDLLT

TOHTT"4406660

CAGAAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCCGCGCCCCCGGTGTGAGGCGGCCTCACAGGGCCGGGTGGGCTGGCGAGCCGACGCGGCGCGGAGGAGGCTGTGAGAGTGTGTGGAACAGGACCCGGGACAGAGGAACCATGCTCCGAGAACCTGAGCACCTTTGCCTGTTGCTGCTATACCTCATCGGGCGGTGATTGCCGGACGAGATTTCTATAAGATCTTGGGGTGCCTCGAAGTGCTCTATAAAGGATATTAAGGACCTATAGGAACTAGCCCTGCA GCTTCATCCCGACCGAACCTTGATGATCACAAGCCAGGAGAAATCCAGGATCTGGGTGCTGCTATGAGGTTCTGTGATAGTGAGAAACGGAACAGTACGATACTTATGGTGAAGAA GGATTAAGATGGTCATCAGAGCTCCCATTGGAGACATTTTTTACACTTCTTTGGGGATT TTGTTTTCATGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATCCAAGAGGAAGTGATA TTATTGTAGATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAATTTTGTGAAGTAGTT AGAAACAAACCTGTGGCAAGCGAGGCTCTGGCAACCGGAAGTCAATTTGTGGCAAGAGAT GCGGACACCCAGCTGGGCCCTGGGCGCTTCCAATAGCAACGAGAGGTGGTCTGCGACGAAT GCCCTAATGTCAAAGTGTGAATGAGAAGCAACGCTGGAAGTAGAAATAGAGCTGGGGTG AGAGACGTCATGGAGTACCCCTTTATTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTGG AGATTTACGTTCCGAATCAAAGTTGTCAAGCACCAATATTTGAAAGGAGAGGAGATGATT TGTACACAAATGTGACAAATCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACT CACTTGGATGGTCACAAGGTACATATTTCCCGGGATAAGATCACCAGGCCAGGAGCGAAGCT ATGGAAGAAAGGGGAAGGGCTCCCCAACTTTGACAACAACATATCAAGGGCTCTTTGATAA TCACTTTTGATGTGGATTTTCCAAAAGAACGTTTAAAGAGGAGGAGAGAAAGGTATCAAA CAGCTACTGAAACAGGGTCAGTGCAGAAGGTATACAATGGACTGCAAGGATATTGAGAGTG AATAAAATTGGACTTTGTTTAAATAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTT TTGTGTGTGTTTTTGTGTTTTATTTTCAATATGCAAGTTAGGCTTAATTTTTTTATCTAATGA TCATCATGAAATGAATAAGAGGGCTTAAGAATTTGTCCATTGCAATTCGAAAAGAATGACC AGCAAAAGGTTTACTAATACCTCTCCCTTTGGGGATTAAATGTCTGGTGCTGCCCGCTGAGT TCAAGAATTAAAGCTGCAAGAGGACTCCAGGAGCAAAAGAAACATATAGAGGGTTGGA GTTGTTAGCAATTTCAATCAAATGCCAACTGGAGAAGTCTGTTTTTAAATACAGCTTTTGTG TATTTTTA

FIGURE 85

MAPQNLS^TFCLLLLYLIGAVIAGRDFYKILGVPSRASIKDIKKAYRKALQLHPDRNPDDFQ
AQEK^FQDLGAAEVLSDSEKRRQYDTYGEGLKGHGQSSHGDI^FSHF^FGDFGFMFGGT^FPRQ^Q
DRNI^FPRGSDI^FIVDLEVTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPRFRQ^Q
MTQEVVCD^ECPNVKLVNEERTLEVEIEP^GVRDGM^EYPF^IGE^GEPHDV^GEGPGL^DLR^FRIK^VV^VK^H
PIFER^RGGDL^LTYNT^ISVLSE^LVGFE^MEDIT^HLDG^HK^VHS^RDK^ITRGAK^LWK^KGEGL^PN^FD^E
NNN^IKGSL^IITFDV^DPE^KQ^LTEA^REG^MI^KQL^LKG^SVQ^KV^NGLQ^Y

Important features:

Signal peptide:

amino acids 1-22

Cell attachment sequence.

amino acids 254-257

Nt-dnaJ domain signature.

amino acids 67-87

Homologous region to Nt-dnaJ domain proteins.

amino acids 26-58

N-glycosylation site.

amino acids 5-9, 261-265

Tyrosine kinase phosphorylation site.

amino acids 253-260

N-myristoylation site.

amino acids 18-24, 31-37, 93-99, 215-221

Amidation site.

amino acids 164-168

FIGURE 86

TGGGACCAGGGAACCCCGGGCCCCCGGTGGAGNGCCTAACAGGCCGGTGGNTGCGACCGAA
GCGGCGGGCGGAGGAGGTTTTGAGGATTTTGGAACAGGACCCGGACAGAGGAACCATGGTT
CCGCAGAACNTGAGCACNTTTTGCCTGTTGNTGNTATACTTCATCGGGGCGGTGATTGCCGG
ACGAGATTTNTATAAGATTTTGGGGTGCCCTNGAAGTGCCTTNTATAAAGGATATTA AAAAGG
CCTATAGGAACTAGCCCTGCAGNTTTATCCCAGCCGAACCCCTGATGATCCACAAGCCCAG
GAGAAATTCAGGATTTGGGTGCTGCTTATGAGGTTNTGTCAGATAGTGAGAAACGGAACA
GTACGATAATTATGGTGAAGAAGGATTAAGATGGTNATCAGAGCTCCCATGGAGACATTT
TTTCACACTTNTTTGGGGATTTTGGTTTCATGTTGGAGGAACCCCTNGTCAGCAAGACAGA
AATATTCCAAGAG

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GGCAGCAGGCGCGGGCGCAGTCGCGGGATGCGCCCGGGAGGCCACAGCCTGAGGCCCTCAGGT
CTCTGTCAGGTGTCGTGGAGGAACCTAGCACCTGCCATCCTCTTCCCCAATTGCCACTTCCA
GCAGCTTTAGCCCATGAGGAGGATGTGACCGGGACTGAGTCAGGAGCCCTCTGGAAGC**ATGG**
AGACTGTGGTGATTGTTGCCATAGGTGTGCTGGCCACCATCTTTCTGGCTTCGTTTGCAGCC
TTGGTGCTGGTTTGCAGGCAGCGCTACTGCCGGCCGCGAGACCTGCTGCAGCGCTATGATT
TAAGCCCATTGTGGACCTCATTGGTGCCATGGAGACCAGTCTGAGCCCTCTGAGTTAGAAC
TGGACGATGTCGTTATACCAACCCCCACATTGAGGCCATTCTGGAGAATGAAGACTGGATC
GAAGATGCCTCGGGTCTCATGTCCACTGCATTGCCATCTTGAAGATTTGTCACACTCTGAC
AGAGAAGCTTGTTGCCATGACAATGGGCTCTGGGGCCAGATGAAGACTTCAGCCAGTGTCA
GCGACATCATTGTGGTGCCAAAGCGGATAGCCCCAGGGTGATGATGTTGTGAAGTCGATG
TACCCTCCGTTGGACCCAAACTCCTGGAGCGACGGAGGACTGCCCTGCTCCTGTCTGTCTAG
TCACCTGGTGCTGGTGACAAGGAATGCCTGCCATCTGACGGGAGGCCTGGACTGGATTGAC
AGTCTCTGTCTGGCTGCTGAGGAGCATTGGAAGTCCTTCGAGAAGCAGCCCTAGCTTCTGAG
CCAGATAAAGGCCCTCCAGGCCCTGAAGGCTTCTGACAGGAGCAGTCTGCAATT**TAG**TGCCT
ACAGGCCAGCAGCTAGCCATGAAGGCCCCTGCCGCCATCCCTGGATGGCTCAGCTTAGCCTT
CTACTTTTTCTATAGAGTTAGTTGTTCTCCACGGCTGGAGAGTTACAGCTGTGTGTCATAG
TAAAGCAGGAGATCCCCGTCAAGTTTATGCCTCTTTTGCAAGTTGCAAACCTGTGGCTGGTGAGT
GGCAGTCTAATACTACAGTTAGGGGAGATGCCATTCACTCTCTGCAAGAGGAGTATTGAAA
CTGGTGGACTGTCTAGCTTTATTTAGCTCACCTAGTGTTTTCAAGAAAATTGAGCCACCGCTT
AAGAAATCAAGAGGTTTCACATTAAATTAGAATTTCTGGCCCTCTCGCATCGGTGCAAGT
TGTGGCAATTCTGATCTGCATTTTCAGAGGAGCAACAATTAAGAACTAAGTAGGGGGTTTC
TTCTTTTGGCAAGACTGTACTCTCTCAGACTGGCCTGTTTTCATTTATTTGTATTATCTGCCT
GGTCCCTGAGCGCTCTGGGTCTCTCCCTCTCCCTTGCAGGTTTGGGTTTGAAGCTGAGGAAC
ACAAAGTTGATGATTTCTTTTATCTTTATGCCTGCAATTTTACCTAGCTACCACTAGGTG
GATAGTAAATTTATACTTATGTTTCCCTCAAAAAAAAAAAAAA

FIGURE 88

METVVIVAIGVLATIFLASFAALVLVCRQRYCRPRDLLQRYDSKPIVDLIGAMETQSEPSEL
ELDDVVITNPHIEAILENEDWIEDASGLMSHCIAILKICHTLTEKLVAMTMGSGAKMKSAS
VSDIIVVAKRISPRVDDVVKSMYPPLDPKLLDARTTALLSVSHLVLTRNACHLTGGLDWI
DQSLSAEEHLEVLREAALASEPDKGLPGPEGFLQEQSAI

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GCTTCATTTCCTCCGACTCAGCTTCCCACCTGGGCTTTCGAGGTGCTTTCGCCGTGTC
CCACCACCTGCAGCCATGATCTCCTTAAACGGACACGCAGAAAAATTGGAATGGGATTAAACAGGA
TTTGGAGTGTTTTTCTGTCTTTTGAATGATTCTCTTTTTTGACAAAGCACTACTGCGTAT
TGGAAATGTTTTATTGTAGCCGGCTTGCTTTTGTAAATGGTTTAGAAAGAACATTAGAT
TCTTCTCCAAAAACATAAAATGAAAGCTACAGGTTTTTTCTGGGTGGTGTATTGTAGTC
CTTATTGTTTGGCTTTGATAGGCATGATCTTCGAAATTATGGATTTTTCTCTGTTCAG
GGGCTTCTTCTGTGCTGTTGTGGCTTTATTAGAAGAGTGCAGTCCTTGGATCCCTCCTAAAT
TTACCTGGAATTAGATCATTTGTAGATAAAGTTGGAGAAAGCAACAATATGGTATAACAACA
AGTGAAATTTGAAGACTCATTTAAAAATATTGTGTTATTTATAAAGTCATTTGAAGAATATTC
GCACAAAATTAAATTACATGAAATAGCTTGTAAATGTTCTTTACAGGAGTTTAAACGTATAG
CCTACAAAGTACCAGCAGCAAATTAGCAAAGAAGCAGTAAAAACAGGCTTCTACTCAAGTGA
ACTAAGAAGAAGTCAGCAAGCAAACCTGAGAGAGGTGAAATCCATGTTAATGATGCTTAAGAA
ACTCTTGAAGGCTATTGTGTGTTTTTCCACAATGTGCGAAACTCAGCCATCCCTTAGAGAA
CTGTGGTGCTGTTTCTTTCTTTTATTTTGAAGGCTCAGGAGCATCCATAGGATTTGCT
TTTTAGAAGTGTCACATGGCAATGGCAAAAAATTTCAGGTGCATGCTATCTGGAAGTGA
TGCATGAATTCGATTGGATTGTGCTATTTTAAAGTATTAAGAACAGGAAACCCCAATTTG
ATGTATGGATTACTTTTTTTGNGCNCAGGGCC

FIGURE 90

MISLTDQTQKIGMGLTGFGVFFLFFGMILFFDKALLAIGNVLEFVAGLAFVIGLERTFRFFFQK
HKMKATGFFLGGVFVVLIGWPLIGMIFEIYGFFLLFRGFFPVVVGFIIRVPVLGSLNLP
RSFVDKVGESNNMV

Important features:

Transmembrane domains:

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

N-myristoylation sites.

amino acids 11-16, 51-56 and 116-121

Aminoacyl-transfer RNA synthetases class-II protein.

amino acids 49-59

90/330-110000

GAAGACGTGGCGGCTCTCGCCTGGGCTGTTTCCCGGCTTCATTCTCCCGACTCAGCTTCCC
ACCN TGGGCTTTCCGAGGTGCTTTCGCCGTGTCCCCACCAC TGCAGCCATGATCTCCTTAA
CGGACACGCAGAAAAATTGGAATGGGATTAACCGGATT TGGAGTGT TTTCTGTCTTTTGGGA
ATGATTCCTTTTTTGACAAAGCACTACTGGCTATTGGAATGTTTATTTGTAGCCGGCTT
GGCTTTTGTAAATGGTTTAGAAAGAACATTAGATCTCTCTTCCAAAAACATAAAATGAAAG
CTACAGGTTTTTTTTCTGGGTGGTGTATTTCAGTCTCTATTGGTTGGCCTTTGATAGGCATG
ATCTCGAAATTTATGAGATT TTTCTCTTGTTCT

FIGURE 92

GGCAGGAGGTGAACCCAGCCGGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAA
GGCTGCCAGGAAGGAGACGCCTTCTGAGTCCTGGATCTTTCTTCCCTTCTGGAATCTTTGA
CTGTGGGTAGTTATTTATTTCTGAATAAGAGCGTCCACGCATC**ATG**GACCTCGCGGACTGC
TGAAGTCTCAGTTTCTGTGCCACCTGGTCTTCTGCTACGTCTTTATTGCCTCAGGGCTAATC
ATCAACACCATTAGCTCTTCACTCTCCTCCTCTGGCCCATTAACAAGCAGCTCTTCCGGAA
GATCAACTGCAGACTGTCTATTGCATCTCAAGCCAGCTGGTGATGCTGCTGGAGTGGTGGT
CGGGCAGGAATGCACCATCTTCAAGGACCCGCGCCTACCTCAAGTATGGGAAGGAAAAAT
GCCATCGTGGTTCTCAACCACAAGTTTGAATTTGACTTTCTGTGTGGCTGGAGCCTGTCCGA
ACGCTTTGGGCTGTAGGGGGCTCCAAGGTCCTGGCCAAGAAAGAGCTGGCCTATGTCCCAA
TTATCGGCTGGATGTGGTACTTCACCGAGATGGTCTTCTGTTCGCGCAAGTGGGAGCAGGAT
CGCAAGACGGTTGCCACCAGTTTGCAGCACCTCCGGGACTACCCCGAGAAGTATTTTTTCTT
GATTCAGTGTGAGGGCACACGGTTACGGAGAAGAAGCATGAGATCAGCATGCAGGTGGCCC
GGGCCAAGGGGCTGCCTCGCCTCAAGCATCACCTGTTGCCACGAACCAAGGGCTTCGCCATC
ACCGTGAGGAGCTTGAGAAATGTAGTTTCACTGTATATGACTGTACACTCAATTTCAGAAA
TAATGAAATCCAACACTGTGGGAGTCTTAACGGAAGAAATACCATGCAGATTTGTATG
TTAGGAGGATCCCACTGGAAGACATCCCTGAAGACGATGACGAGTCTCGGCCTGGCTGCAC
AAGCTCTACCAGGAGAAGGATGCCTTTCAGGAGGAGTACTACAGGACGGGCACCTTCCGAGA
GACGCCCATGGTGCCCCCGCGGCCCTGGACCTCGTGAACCTGGCTGTTTTGGGCTCGC
TGGTGCTCTACCTTTCTTCCAGTTCCTGGTCAGCATGATCAGGAGCGGGTCTTCCCTGACG
CTGGCCAGCTTCATCCTCGTCTTCTTGTGGCCTCCGTGGGAGTTCGATGGATGATTGGTGT
GACGGAATTGACAAGGGCTCTGCCTACGGCAACTCTGACAGCAAGCAGAACTGAATGAC**T**
GACTCAGGGAGGTGTACCATCCGAAGGGAACCTTGGGGAACCTGGTGGCCTCTGCATATCCT
CCTTAGTGGGACACGGTGACAAAGGCTGGGTGAGCCCTGCTGGGCACGCGGAAGTCACGA
CCTCTCCAGCCAGGAGTCTGGTCTCAAGCCGGATGGGAGGAAGATGTTTTGTAATCTTT
TTTTCCCATGTGCTTTAGTGGGCTTTGGTTTTCTTTTTGTGCGAGTGTGTGTGAGAATGGC
TGTGTGGTGAGTGTGAACTTGTCTGTGATCATAGAAAGGTATTTTAGGCTGCAGGGGAG
GGCAGGGCTGGGGACCGAAGGGGACAAGTTCCCTTTTCATCCTTTGGTGCTGAGTTTTCTGT
AACCTTGGTTGCCAGAGATAAAGTGAAAGTGCTTTAGGTGAGATGACTAAATTATGCCTC
CAAGAAAAAAATTAAGTGCTTTTCTGGGTCAAAAAAAAAA

MDLAGLLKQSFCHLVFCYVFASGLIINTIQFLTLLLPINKQLFRKINCRLSYCISSQLV
MLLEWWSGTECTIFTDPRAYLKYGKENAIVLVNHKFEIDFLCGWSLSERFGLGGSKVLAKK
ELAYVPIIGWMWYFTEMVFCRKEQDRKTVATSLQHLRDYPEKYFFLIHCEGTRFTEKKHE
ISMQVARAKGLPRLKHLLPRTKGFAITVRSRLNVSAVYDCTLNFRNNENPTLLGLVNGKK
YHADLYVRRIPLEDIPEDDDECSAWLHKLYQEKDAFQEEYYRTGTFPETPMVPPRRPWTLVN
WLFWASLVLYPFFQFLVSMIRSGSSLTASFILVFFVASVGRWMIGVTEIDKGSAYGNSDS
KQKLN

FIGURE 94

CTGAGCGGCGGTAGC**ATG**GAGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCG
 GCGCACTCGCTTTCCAGCACTCAACACGGACTCGGACACGGAAGGTTTTCTTCTGGGGAA
 GTAAAGGTTGAAGCCAAAGAACAGCATTACTGATTCCCAAATGGATGATGTTGAAGTTGTTTA
 TACAATTGACATTCAGAAATATATTCCATGCTATCAGCTTTTTAGCTTTTATAATTCTTCAG
 GCGAAGTAAATGAGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGT
 TGGTACAAATTCGTCGTCATTTCAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAA
 AAACCTGCAGGAGCATTTTTCAAACCAAGACCTTGTTTTCTGCTATTAAACCAAGTATAA
 TAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCTTATATAAACCTCAAAAAGGACTT
 TTTCACAGGGTACCTTTAGTGGTTGCCAATCTGGGCATGTCTGAACAACCTGGGTTATAAAC
 TGTATCAGGTTCTGTATGTCCACTGGTTTTAGCCGAGCAGTACAAACACACAGCTCTAAAT
 TTTTTGAAGAAGATGGATCCTTAAAGGAGGTACATAAGATAAATGAAATGATGCTTCATTA
 CAAGAGGAATTAAGAGTATATGCAAAAAGTGGAAGACAGTGAACAAGCAGTAGATAAACT
 AGTAAAGGATGTAACACAGATTAACGAGAAATTGAGAAAAGGAGAGGAGCAGATTCAGG
 CAGCAAGAGAGAAGAATCCAAAAAGACCCCTCAGGAGAACATTTTCTTTGTGAGGCATTA
 CGGACCTTTTTTCCAAATTCGAATTTCTTCATTATGTGTTATGTCTTTAAAAATAGACA
 TGTTTCTAAAGTAGCTGTAACATAACACCACATCTCGATGTAGTAGACAATCTGACCTTAA
 TGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCACAAATCATTAAAGCAT
 AAAGCCTTAGACTTAGATGACAGATGGCAATTCGAAGATCTCGGTTGTTAGATACACAAGA
 CAAACGATCTAAAGCAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAATGAGCAGCC
 CAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTTGGTGAATATTACGGTCTCCTACA
 TTT**TGAT**CCTTTTAACTTACAAGGAGATTTTTTATTGGCTGATGGGTAAAGCCAAACAT
 TTCTATTGTTTTTACTATGTTGAGCTACTGCAGTAAGTTCATTGTTTTTACTATGTTTAC
 CTGTTTGCAGTAATACAGATAACTCTTAGTGCATTACTTCACAAAGTACTTTTTCAAAC
 ATCAGATGCTTTTATTCCAAACCTTTTTTTCACCTTTCCTAAGTTGTTGAGGGGAAGGCT
 TACACAGACACATTCCTTAGAATTGGAAGTGAAGACAGGCACAGTGGCTCACACCTGTAA
 TCCCAGCACTTAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCC
 TGGGCAACGTATTGAGACCATTGTCTATTAATAAATAAATGGAAGCAAGAATAGCCTTAT
 TTCAAAATATGGAAGAAATTTATATGAAAATTTATCTGAGTCATTAATTTCTCCTTAAG
 TGATACTTTTTTAGAAGTACATTATGGCTAGAGTTGCCAGATAAATGCTGGATATCATGCA
 ATAAATTTGCAAAACATCATCTAAATTTAAAAAAAAAAAAAAAAAAAAA

MEGESTSAVLSGFVLGALAFQHLNTDSDTEGFLGGEVKGEAKNSITDSQMDDEVVYITIDIQ
KYIPCYQLFSFYNSSGEVNEQALKKILSNVKKNVVGWYKFRHSDQIMTFRERLLHKNLQEH
FSNQDLVFLLLTPSIITESCSTHRLHSLYKPGKGLFHRVPLVVANLGMSEQLGYKTVSGSC
MSTGFSRAVQTHSSKFFEEEDGSLKEVHKINEMYASLQOEELKSICKKVEDSEQAVDKLVKDVN
RLKREIEKRRGAQIQAAAREKNIQDKPQENIFLCQALRTFFPNSFHLSCVMSLKNRHSVSS
CNYNHLDVDVNDLTLMEVHTIDPEASPDENIQCIIKKHALDLDDRQWFKRSRLLDQDKRSKA
NTGSSNQDASKMSSPDEETEEKMGFGEYSRPTF

GGCACAGCGCGCGGGGAGGGCAGAGTCAGCCGAGCCAGTCCAGCCGGACGAGCGGACAGCGAGCGGAGCGAGCGGAGCGAC
CCAGAGCGAGCGGCGAGGCAAGCGCGCGCGCGCCGACCAACCCCTCTCGGCTCCCGCGGGCCCTGCCACCTCTCCCTCT
CCTTCCCGCGGCTCCCGCGCTCTCGCGCGCAGCTCAGCTTCCGGGTTTGGTGCGCGCGAAACCCGGAGTCCACCA
CGCGCGGCTCTGCTTCTCTGGGCGCGCGCGCGCTCCAGCGCTCTCTTCTCCCTCGGCGCGCGCTCGGCAC
GGGAGGCTGCTGCTGACGGCAGCGACCTACTTCTTCCGCCGCGCTCTCTCCGCTGCTCGCTCTTCTCCAC
CAACTCCAATCTCTTCTCCCTCAGCTCTCAGCTGCTAGTCCCGCACTCCGCGAGCCCTCGCGCGCTCGGCTA
CGCGCTTCCGCTCCGGTCCAAAGGTGGAAAGCTCGCCCGCGCCGACCAATGCGAGCTGCGCTTGC
CGCGTCTCTCTGCACCTCGGAGCTCTCAGCGCGCGCTGCTGGCTCGCGAGTCAAGTCAAAAAGTCTCGG
AGCTGCAGCTCTTTAGCTGTCCAAAGCTCTCAACAAGACGATGCCCTCCAGCAAGTCAACGCTGATCAT
TTGAAGTCTGTCCCGACGCTTACTCTGCTGCTCAAGAGATGGAGGAAGTACAGTCTCAAAAGTAAAGA
TGATTTCAAAGTGTGGTCAAGCAACGATGCAATCATTTGAAGCTCTTCTGCTACGTTCAAGAAAGTTT
ATAAATCTTCAAAGACTACTTGAATACGAGAGAAATCTCGATGATGTTTGTGAGACATATGGCCAT
TTATACGACAAAATTTGAGTATTTAAAGACTCTTTGTAAGTGAAGCTTACTAGCTGGTGGAAATGT
GAACCTGGAGAAATCTCAATAGCACTCTGGGCTCGCCTCTGGAGCGGATGTTCCGCTGGTGAATCCGAT
AACACTTTACAGTGTGATGATCTGGAATGTGTGAGCAAGTATACGGAAGCTGAAGCCCTCGAGATGTCCCT
CGAAATTTGAAGCTCCAGGTTACTCTGCTGTTTGTAGCAAGCCGCTACTTTCGCTCAAGGCTTACGCGTTCGGG
AGATGTCGTGACAAGTCTCTCGTGGTAAACCCACAGCCCACTGACCACTGCCCTGTGAAGATGATCAT
CTCCCACTCGCGGGTCTCGTGACTTGAGAAGCATTTACAATCACTGCTCAAACTCATGAGAGGCTGTGA
GCCAAGCCGGGGATCTCGATTTGAATGGAACATTTCAAGTGTCTATGCTGATGTGGCAGAGGCTTGA
GGGCTCTTTCAAGATTGAATCGGTGATGGATCCCATCGATGTGAAGATTTCTGATGCTTATGAACATCGAG
ATAATGTTCTCAAGTGTCTCAAGGTTTCTCGAGGTTTCTCGAGGATGTGACACCGACTGCTGGGAGAGT
TCTCGTTCATCTCTCGAAGTGCCTCTCAGTCTCGCTTCAGCACAACATCCACCGAGGACGCCCAACCA
AGTGCGCATGTTTGGACCGCTGTTTACTGATGTCAAGGAAACTGAACACGGCAACAACCAAGATCG
GGTTGACACCGAACAACGACATGATGATCTCTGCAATCATGCTCTTCGATGATGACCAAGCAATGA
AGAATGACATACATGAAGGACAGCTGGACCTCTTTGATGATTCAGTGAAGAAATAGTGGAGAGGAATGGAAT
GGCTGTGAGTATCAGCAGTGCCCTTCAGAGTTTGACTATAGTGCACTGACATGCTGGGAGAGTGC
GAAAGCCGACATGCTGGTGTCCGCTCGGGGACAGCGCACTCTCTCACTGCTTCTGCACTCTGTTCCCT
TTATGACGAGAGATGGAGTAATACTCAAACTCGAGAAAGATGTTCTCAAAAAGTTAAAGGACACAGTT
ATCACTTTTCTACATCTAGTGAAGTGGCTTTTAAATGAATGGACAACATGTACAGTTTCTTACTATGTGC
CACTGGTTTAAAGAGTGTCACTTTGTTTCTTCACTCAGTTTGGGAGAAAGGACATGTGCATGAGTTGT
TCTGCTGCCCAACCAATCTTAAAGCGTGGCTAAACCTGTAGTACAGACTATAGTTAGTTGTGATTTGTGA
TTTATACATCTATATTTGTTTGTATGTTTCTTCTTCTGTTTGGGTTTCTTCTTCAACTGTATCTCT
CGCTCTGTTTCTTCAAGCAAGAACAGGCTCCCTCTTGCGCATGATCATGTATTTCTGAAATATTAATA
GCTGTACAGAACGAGGTTTATTTATCTATGTTATCTTATTAAGAGAAAGGCCCAAAAGC

FIGURE 97

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRLYVSKGFKNKDAPLHEINGDHLKICPQ
GSTCCSQEMEKEYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMF
VKTYGHLYMQNSSELFKDLFVELKRYVVGNNLEEMLNDFWARLLERMFRLVNSQYHFTDEY
LECVSKYTEQLKPFQDVPRKLKQVTRAFVAARTFAQGLAVAGDVVSKVSVVNPTAQCTHAL
LKMIYCSHCRGLVTVKPCYNYCSNIMRGCLANQGDLD FEWNNFIDAMLMVAERLEGPFNIES
VMDPIDVKISDAIMMQDNSVQVSQKVFQCGCPPKPLPAGRISRSESASFARFRPHHPEE
RPTTAAGTSLDRLVTDVKEKLQAKKFWSSLPSNVCNDERMAAGNGNEDDCWNGKGKSRYLE
AVTGNGLANQGNNPEVQVDTSKPDILILRQIMALRVMTSKMKNAYNGNDVDFDISDESSGE
GSGSGCEYQQCPSEFDYNATDHAGKSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

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FIGURE 98

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCT
GACCTGAGTCATCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAA
GCAACTTACAGCTGCACCGACAGTTGCGATGAAAAGTTCTAATCTCTTCCCTCCTCCTGTTGC
TGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTGCCAGAGGCCAC
AGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAA
AGATTGGTTCTGAGAGCCCCGAGAAGAAAATTATGACAGTGTCTGGGCTGCCAAAGAAGC
AGTGCCCTGTGATCATTTCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGA
AAGCCAAACAAGCATTCCAGAGCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTT
TGCTCTGCCTTTGTAGGAGCTCTGAGCGCCCACTCTTCCAATTAAACATTCTCAGCCAAGAA
GACAGTGAGCACCTACCAGACACTCTTCTTCTCCACCTCACTCTCCCACTGTACCCACC
CCTAAATCATTCAGTGCTCTCAAAAGCATGTTTTCAAGATCATTTGTTTGTGTGCTCTC
TCTAGTGTCTTCTCTCGTCAGTCTTAGCCTGTGCCCTCCCCTTACCCAGGCTTAGGCTT
AATTACCTGAAAGATTCCAGGAACTGTAGCTTCCTAGCTAGTGTCAATTTAACCTTAAATGC
AATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTTAAATGTCAAAAAAAAAAAAAAAAAA

FIGURE 99

MKVLISLLLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRR
KFMTVSGLPKKQCPDHFKGNVKKTRHQRHHRKPNKHSRACQQFLKQCQLRSFALPL

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FIGURE 100

AATGGCTGTCTTAGTACTTCGCCTGACAGTTGTCCTGGGACTGCTTGCTTATTCCTGACCT
GCTATGCAGACGACAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCA
AAGCCAGACTTCCCCAAATTCTTAAGCCTCCTGGGCACAGAGATCATTGAGAATGCAGTCGA
GTTTCATCCTCCGCTCCATGTCCAGGAGCACAGGATTTATGGAATTTGATGATAATGAAGGAA
AACATTTCATCAAAG**TGA**CATCCTCAGGACACACCCATGTGGCTCCTGGACAATCCAAGAGCA
GCCAAATCCTGCTTTTCCAGTTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAAC
TCCCAACGAGTTCTCAGGATTCAGGCTCTGGCTTCAACCAAAACAGAACTCATTTTGAACACC
CTGACTGCATTTTTGCTTTTGAAGTTAGAATAAATATGGCGCTTTGGGATCACATAGTTG
ATGGAGAGGAAA

101/330

FIGURE 101

MAVLVLRLTVVLGLLVFLTCYADDKPKDPDDSGKDPKPDFPKFLSLLGTEIIEHAVE

FILRSMRSTGFMEDDNEGHSSK

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FIGURE 102

GGAGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCT
 CAGAGCTGGTCTGCCATGGACATCCTGGTCCCACTCCTGCAGCTGCTGGTGTCTTCTTAC
 CCTGCCCCTGACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCTGTGCAAAAGCTACTTCC
 CCTACCTGATGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAG
 CTCTTCAGCCAGATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGCTGGG
 CTGCGGAACCGGAGCCAACTTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACC
 CAAATCCCCACTTTGAGAAGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATAT
 GAGCGGTTTGTGGTGGCTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGT
 GGTGGTCTGCACTCTGGTGTCTGTCTGTGCAGAGCCCAAGGAAGGTCCTGCAGGAGGTCC
 GGAGAGTACTGAGACCGGGAGGTGTGCTCTTTTCTGGGAGCATGTGGCAGAACCATATGGA
 AGCTGGGCCCTTCATGTGGCAGCAAGTTTTCGAGCCCCACCTGGAACACATTGGGGATGGCTG
 CTGCCCTACCAGAGAGACCTGGAAGGATCTTGAGAAGCCCCAGTTCTCCGAAATCCAAATGG
 AACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTC
 AAACAATCTTTCCCAAGCTCCAAGGCACTCATTGTCTCTTCCCAGCCTCCAATTAGAACA
 AGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACCTAGCAGAATGAGAGAAGACATT
 CATGTACCACCTACTAGTCCCTCTCTCCCAACCTCTGCCAGGCAATCTCTAACTTCAATC
 CCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGGAAACACTAGGACCC
 TGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCCTCCCAATGTTGTC
 CCTTTCCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACACCCATGCGT
 CTCTAGGAAGTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGACCCTCT
 CTCCCACCTACCACCTTCTTCTGAGCTGGGGGCACCAGGGAGAATCAGAGATGCTGGGGAT
 GCCAGAGCAAGACTCAAGAGGCAGAGGTTTTGTTCTCAATATTTTTTAATAAATAGACGA
 AACCACG

FIGURE 103

MDILVPLLLQLLVLLLTLPPLHMLALLGCWQPLCKSYFPYLMAVLTPKSNRMESKKRELFSQI
KGLTGASGKVALLELGGGTGANFQFYPPGCRVTLCDPNPHFEKFLTKSMAENRHLYQYERFV
APGEDMRQLADGSMDEVVCTLLRLCSVQSPRKVLQEVRRVLRPGGVLFWEHVAEYPGSWAF
WQVQFEPTWKHIGDGCLTLRETWKDLENAQFSEIQMERQPPPLKWLFPVGHIMQKAVKQSPF
SSKALICSPSLQGLQEQATHQPIYPLPLRGT

[illegible]

FIGURE 104

GTGGGATTTATTTGAGTGCAAGATCGTTTTCTCAGTGGTGGTGGAAAGTTGCCTCATCGCAGG
 CAGATGTTGGGGCTTTGTCCGAACAGCTCCCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAA
 ACTAATATTTATATGACAGAAGAAAAAGATGTTCATTCCGTAAAGTAAACATCATCATCTTGG
 TCCTGGCTGTTGCTCTCTTCTTACTGGTTTTGCACCATAACTTCCTCAGCTTGAGCAGTTTG
 TTAAGGAATGAGGTTACAGATTTCAGGAATTGTAGGGCCTCAACCTATAGACTTTGTCCCAA
 TGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATCTG
 AAGACAGGCTTGGGGGGGCCATTGCAGCTATAAACAGCATTTCAGCACAACTCGCTCCAAT
 GTGATTTTCTACATTGTTACTCTCAACAATACAGCAGACCATTCTCCGGTCTGGCTCAACAG
 TGATTCCCTGAAAAGCATCAGATACAAAATTGTCAATTTTGACCTAACTTTTGGAAGGAA
 AAGTAAAGGAGGATCCTGACCAGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTAC
 TTGCCAATTCTGGTTCCAGCGCAAGAAGGCCATATACATGGATGATGATGTAATTGTGCA
 AGGTGATATCTTGCCCTTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAG
 AAGATTGTGATTTCAGCTCTACTAAAGTTGTCTCCGTGGAGCAGGAAACAGTACAATTAC
 ATTGGCTATCTTGACTATAAAAAGGAAAGAAATTTCGTAAGCTTTCCATGAAAGCCAGCACTTG
 CTCATTTAATCCTGGAGTTTTTGTGCAAACCTGACGGAATGGAACGACAGAATATACTA
 ACCAACTGGA AAAATGGATGAACTCAATGTAGAAGAGGGACTGTATAGCAGAACCCTGGCT
 GGTAGCATCACAACACCTCCTCTGCTTATCGTATTTTATCAACAGCACTCTACCATCGATCC
 TATGTGGAATGTCCGCCACCTTGGTTCCAGTGCTGGAAAACGATATTCACCTCAGTTTGTA
 AGGCTGCCAAGTTACTCCATTGGAATGGACATTTGAAGCCATGGGGAAGGACTGCTTCATAT
 ACTGATGTTTGGGAAAAATGGTATATTCAGACCCAACAGGCAAATTC AACCTAATCCGAAG
 ATATACCGAGATCTCAAACATAAAGTGA AACAGAATTTGAACTGTAAGCAAGCATTCTCAG
 GAAGTCTGGAAGATAGCATGCATGGGAAGTAACAGTTGCTAGGCTTCAATGCCTATCGGTA
 GCAAGCCATGGA AAAAGATGTGTAGCTAGGTAAAGATGACAACTGCCCTGTCTGGCAGTC
 AGCTTCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGTGTTTCTT
 ACTACAAATGCTGAATGACTGGAAAGAAGAACTGATATGGCTAGTTTCAAGTGTGTTACAGA
 TAATTCAAACCTGCTGTTGGTTTTTAATTTTGTAACTGTGGCCTGATCTGTAATAAACTT
 ACATTTTTT

FIGURE 105

MSFRKVNIIILVLAVALFLLVLHNFSLSSLLRNEVTDSGIVGPQPIDFVPNALRHAVDGR
QEEIPVVIAASEDRLGGAIAAINSIOHNTSRNVIFYIVTLNNADHLRSWLNSDSLKSTRYK
IVNFPDKLLEGKVKEDDPQGESMKPLTFAFYFLPILVPSAKKAIYMDDDVIVQGDIILALYNT
ALKPGHAAAFSEDCDSASTKVVIRGAGNQYIYIGYLDYKKIRFKLQSMKASTCSFNPGFVFA
NLTEWKQRQNTINQLECKMWKLVEEGLYSRTLAGSITTPPELLIVFYQKSHSTIDPMWNVRHLGS
SAGKRYSPQFVKAALKLHWNHGLKPWGRTASYTDVWEKWIYPDPTGKFNLIRRYTEISNIK

[illegible]

FIGURE 106

TGGTTTTTGCCCCATAAATTCCTCAGCTTGAGCAGTTTGTTAAGGAATGAGGTTACAGATT
CAGGAATTNTAGGNCCTCAACCTNTAGANTTTGTCCCAAATGTTCTCCGACATGCAGTAGAT
GGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATNTGAAGACAGGCTTGGGGGGGCCAT
TGCAGCTATAAACAGCATTTCAGCACAACACTCGNTCCAATGTGATTTTCTACATTGTTACTC
TCAACAATACAGCAGACCATNTCCGGTCCTGGNTCAACAGTGATTCCCTGAAAAGCATCAGA
TACAAAATTGTCAATTTTGACCCTAAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCA
GGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGTTCACGCG
CAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCAAGGTGATATCTTGCCCTTTAC
AATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTCAGCCTCTAC
TAAAGTTGTCATCCGTGGAGCAGGAAA

FIGURE 107

CGACGCTCTAGCGGTTACCGCTGCGGGCTGGCTGGGCGTAGTGGGCGTGC GCGGCTGCCACG
 GAGCTAGAGGGCAAGTGTGCTCGGCCAGCGTGCAGGGAACGCGGGCGGCCAGACAACGGGC
 TGGGCTCCGGGGCTGCGGCGCGGGCGCTGAGCTGGCAGGCGGGTCGGGGCGCGGGCTGCA
 TCCGCATCTCCTCCATCGCCTGCAGTAAGGCGGGCGCGGCGAGCCTTTGAGGGGAACGACT
 TGTGCGAGCCCTAACAGGGGTGTCTCTGAGCCTGGTGGGATCCCGGAGCGTCACATCACT
 TTCCGATCACTTCAAAGTGGTTAAAACTAATATTTATATACAGAAGAAAAAGATGTCATT
 CCGTAAAGTAAACATCATCATCTTGGTCTTGGGCTGTTGCTCTCTTCTTACTGGTTTTGCAC
 CATAACTTCTCAGCTTGAGGCACTTTGTTAAGGAATGAGGTTACAGATTGAGGAATTGTAG
 GGCTCAACCTATAGGACTTTGTCCCAAATGCTCTCCGACATGCAGTAGATGGGAGACAAGA
 GGAGATTCCGTGTGGTCATCGCTGCATCTGAAGACAGGCTTGGGGGGGCCATTGCGAGCTATAA
 ACAGCATTACGACACAACACTCGCTCCAATGTGATTTTCTACATTGTTACTCTCAACAATACA
 GCAGACCATCTCCGGTCTGGGCTCAACAGTGATTCCTGAAAAGCATCAGATACAAAATTG
 TCAATTTTGACCTTAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCAGGGGAATCC
 ATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAAATCTGGGTTCCAGCGCAAGAAGG
 CCATATACATGGATGATGATGTAATTGTGCAAGGTGATATCTTGCCCTTTACAATACAGCA
 CTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTGAGCTCTACTAAAGTTGT
 CATCCGTGGAGCAGGAAACCAGTACAATTACATTGGCTATCTTGACTATAAAAAGGAAAGAA
 TTCGTAAGCTTTCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTTTGTGTCAAAC
 CTGACGGAATGGAACGACAGAAATATAACTAACCAACTGGAAAAATGGATGAACTCAATGT
 AGAAGAGGGACTGTATAGCAGAACCCCTGGCTGGTAGCATCACAAACCTCCTCTGCTTATCG
 TATTTTATCAACAGCACTCTACCATCGATCCTATGTGGAATGTCGCCACCTTGGTTCCAGT
 GCTGGAACCATGATATTCACCTCAGTTTGTAAAGGCTGCCAAGTTACTCCATTGGAATGGACA
 TTTGAAGCCATGGGAAGGACTGCTTCATATACTGATGTTTGGGGAATAATGTTATATCCA
 GACCCAACAGGCAATTTCAACCTAATCCGAAGATATACCGAGATCTCAACATAAAGTGAAA
 CAGAATTTGAACTGTAAGCAAGCATTCTCAGGAAGTCTGGAAGATAGCATGCGTGGGAAG
 TAACAGTTGCTAGGCTTCAATGCCTATCGGTAGCAAGCCATGGAAAAAGATGTGTCAGCTAG
 GTAAAGATGACAACTGCCCTGTCTGGCAGTCAGCTTCCAGACAGACTATAGACTATAAAT
 ATGTCTCCATCTGCCTTACCAAGTGTCTTCTTACTACAATGCTGAATGACTGGAAAGAAGAA
 CTGATATGGCTAGTTCAGCTAGCTGGTACAGATAATTCAAAAGTGTGTTGGTTTTAATTTT
 GTAACCTGTGGCCTGATCTGTAATAAACTTACATTTTCAATAGGTAATAAAAAAAAAAAAA
 AAAAAA

FIGURE 108

CTGCAGGTAGACATCTCCACTGCCCCAGGAATCACTGAGCGTGCAGACAGCACAGCCTCCTCT
GAAGGCCGCCCATAACCAGAGTCCTGCCTCGGCATGGGCCTCACCATTGAGGCAGCTCCACTG
TCTGTGCTGGTCTGAGGGTGTGCTGCCTGT**CATG**GGGGCAGCCATCTCCCAGGGGGCCCTCATC
GCCATCGTCTGCAACGGTCTCGTGGGCTTCTTGCTGCTGCTGCTCTGGGTCACTCTGCTG
GGCCTGCCATTCTCGTCTGCCGACGTTGACTCTCTCTCTGAATCCAGTCCCAACTCCAGCCC
TGGCCCCCTGTCTGAGAAGGCCCCACCACCCAGAGCCAGCCATGAAGGCAGCTACCTGC
TGCAGCCCTGAAGGCCCTGGCCTAGCCTGGAGCCCAGGACCT**TAA**GTCCACCTCACCTAGAG
CCTGGAATTAGGATCCAGAGTTCAGCCAGCCTGGGGTCCAGAACTCAAGAGTCCGCCTGCT
TGGAGCTGGACCCAGCGGCCAGAGTCTAGCCAGCTTGGCTCCAATAGGAGCTCAGTGGCCC
TAAGGAGATGGGCCTGGGGTGGGGCTTATGAGTTGGTGCTAGAGCCAGGGCCATCTGGACT
ATGCTCCATCCCAAGGGCCAAGGGTCAGGGGCCGGGTCCACTCTTCCCTAGGCTGAGCACC
TCTAGGCCCTCTAGGTTGGGGAAGCAAACCTGGAACCCATGGCAATAATAGGAGGGTGTCCAG
GCTGGGCCCTCCCCTGGTCTCCAGTGTTGCTGGATAATAAATGGAACATATGGCTCTAA
AAAAAAAAAAAAAAAAA

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FIGURE 109

MGAATSQGALIAIVCNGLVGFLLLLWVILCWACHSRLPTLTLSLNPVPTPALAPVLRPHH
PRSPAMKAATCCSPEGWPWSLEPRT

109/330
MGAATSQGALIAIVCNGLVGFLLLLWVILCWACHSRLPTLTLSLNPVPTPALAPVLRPHH
PRSPAMKAATCCSPEGWPWSLEPRT

FIGURE 110

GTTTGAATTCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCA
 GTTCCTCCAAGCAAGTCATTTCCCTATTTTAACCGATGTGTCCTCAAACACCTGAGTGCTA
 CTCCCTATTGTCATCTGTTTTGATAAATGATGTTGACACCCCTCCACCGAATTCTAAGTGGA
 TCATGTCGGGAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGTCTTTGGCC
 ATGATGTTTTACCTTCAGATTCAACACCCTTCTGGTTCACATTTTCATTTTCATTTGGTTAT
 TTTGGGATTGTTGTTTGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACC
 TCAGCATAGAATTGGACACAGAAAGGAAAAATATGAAGTGCCTGCTGGGGTTTGCTATCGTA
 TCCACAGGCATCAGGCAGTGTCTGCTCGTCTTGATTTTTGTTCTCAGAAAGAGAATAAAAT
 GACAGTTGAGCTTTTCCAAATCACAATAAAGCCATCAGCAGTGTCTCCCTTCTGCTGTTCC
 AGCCACTGTGGACATTGGCCATCCTCATTTTCTTCTGGGTCTCTGGGTGGCTGTGCTGCTG
 AGCCTGGAACTGCAGGAGCTGCCCAGGTATGGAAGCGGCCAAGTGGAAATATAAGCCCT
 TTCGGGCATTTCGGTACATGTGGTCTGACCATTTAATTGGCCTCATCTGGACTAGTGAATTC
 TCCTTGCCTGCCAGCAATGACTATAGCTGGGGCAGTGGTTACTTGTTATTTCAACAGAAGT
 AAAAAATGATCCTCCTGATCATCCCATCCTTCTGCTCTCTCCATTCTCTTCTTCTACCATCA
 AGGAACCGTTGTGAAAGGGTCATTTTTAATCTCTGTGGTGAGGATTCCGAGAATCATTTGTCA
 TGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCATTGTCCAGGTACCTGTTCCGA
 TGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTCAACCAGAATGCATA
 TACTACAACCTGCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGCATTCAAAATCT
 TGTCCAAGAACCTCAAGTCACTTTACATCTATTAAGTCTTTGGAGACTTCATAATTTTTCTA
 GGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACTACAATCG
 GGCAATCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTGCCTACTTAGTAGCCC
 ATAGTTTTTTATCTGTGTTTGAAGTGTGCTGGATGCACTTTTCTGTGTTTTGCTGTTGAT
 CTGGAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTT
 CGTAAAAGGAGACAACAAATTAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAGGA
 ATGAGGAGGGAACAGAACTCCAGGCCATTGTGAGATAGATACCATTTAGGTATCTGTACCT
 GGAAACATTTCTTCTAAGAGCCATTTACAGAATAGAAGATGAGACCACTAGAGAAAAGTT
 AGTGAATTTTTTTTTTAAAGACCTAATAAACCCATTCTTCTCTCAAAA

FIGURE 111

MSGRDTILGLCILALSLAMMFTFRFITLLVHIFISLVILGLLFVCGVLWWLYDYDTNDL
SIELDTERENMKCVLGFIVSTGITAVLLVLI FVLKRRIKLTVELFQITNKAISSAPFLLFQ
PLWTFAILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFI
LACQQMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPRIIVM
YMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFCTSAKDAFKIL
SKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAFQVWAVPLLVAFFAYLVAH
SFLSVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRN
EEGTELQAIVR

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FIGURE 112

GTTCGATTAGCTCCTCTGAGAAGAAGAGAAAAGGTTCTTGGACCTCTCCCTGTTTCTTCTCTT
 AGAATAATTTGTATGGGATTTGTGATGCAGGAAAGCCTAAGGGGAAAAAGAAATATTCATTCTCG
 TCTGGTGAATAATTTTGAATAAAATTCCTTCTTCAACAAGGGTGTCAATCTGATATTT
TATGAGGACTGTTGTTCTCACTATGAAGGCATCTGTTATTGAAATGTTCTTGTGCTGG
 TGACTGGAGTACATTCAAAACAAAGAAACGGCAAAGAGATTAAAAGGCCAAAGTTCACTGTTG
 CCTCAGATCAACTGCGATGTCAAAGCCGGAAGATCATCGATCCTGAGTTCATTGTGAAATG
 TCCAGCAGGATGCCAAGACCCCAATACCATGTTTATGGCACTGACGTGTATGCATCCTACT
 CCAGTGTGTGTGGCGCTGCCGTACACAGTGGTGTGCTTGATAATTGAGGAGGGAAAACTATT
 GTTCGGAAGGTTCTGGACAGTCTGGTTACAAAGGGAGTTATTCCAACGGTGTCCAATCGTT
 ATCCCTACCAGATGGAGAGAATCCTTTATCGTCTTAGAAAGTAAACCCAAAAAGGGTGTAA
 CCTACCCATCAGCTCTTACATACTCATCATCGAAAAGTCCAGCTGCCCAAGCAGGTGAGACC
 ACAAAGCCATCAGAGGCCACCTATTCAGGGGACAACCTGCACAGCCGGTCACTCTGATGCA
 GCTTCTGGCTGTCACTGTGAGCTGTGGCCACCCCACTTGGCAAGGCCATCCCTCTCTG
 CTGCTTCTACCAACAGCATCCCCAGACCAATCAGTGGGCCACAGGAGCCAGGAGATGGAT
 CTCTGGTCCACTGCCACCTACACAAGCAGCCAAACAGGCCCAGAGCTGATCCAGGTATCCA
 AAGGCAAGATCCTTCAGGAGCTGCCCTCCAGAAACCTGTTGGAGCGGATGTGACGCTGGGAC
 TTGTTCCAAAAGAAAGATTGAGCACACAGTCTTTGGAGCCAGTATCCCTGGGAGATCCAAAC
 TGCAAAATGTACTGTCTGTTTTAATTGATGGGAGCACAGCATTGGCAACCGCGATTCGG
 AATCCAGAAGCAGCTCTGGCTGATGTTGCCAAGCTCTTGACATTGGCCCTGCCGTTCCAC
 TGATGGTGTGTTCCAGTATGGAGACAACCTGCTACTACTTTAACCTCAAGACACACAG
 AATTCTCGAGATCTGAAGACAGCCATAGAGAAAATTACTCAGAGAGGAGGACTTTCTAATGT
 AGGTGGGCCATCTCCTTTGTGACCAAGAACTTCTTTCCAAAGCCAATGGAACAGAAAGCG
 GGCTCCCAATGTGGTGGTGGTATGGTGGATGGCTGGCCACGGACAAGTGGAGGAGGT
 TCAAGACTTGGCAGAGAGTCAGGAATCAACATTTTCTTCATCACCATTGAAGGTGCTGCTGA
 AAATGAGAAGCAGTATGTGGTGGAGCCCACTTTGCAAAACAAAGCCGCTGTGCAGAACAAACG
 GCTTCTACTCTGCCAGTGCAGAGCTGGTTTGGCCTCCACAAAGACCTTCGAGCCTCTGGTG
 AAGCGGGTCTGCGACATGACCGCTGGCCTGCAGCAAGACCTGCTTGAATCGGCTGACAT
 TGGCTTCGTCTCGACGGCTCCAGCAGTGTGGGACGGGCAACTTCGCAACCGTCCCTCCAGT
 CAGTACACCTACGAACAGCGGCTGGAGTTTGGGTTGCACAAGTACAGCAGCAACGCTGACAT
 CCTCAACGCACTCAAGAGGTTGGGCTACTGGAGTGGTGGCACCAGCAGCGGGGCTGCCATCA
 ACTTCGCGCTGGAGCAGCTCTTCAAGAAGTCCAAGCCCAACAAAGAGGAAGTTAATGATCCTC
 ATCACCAGCGGGAGGTCTTACGACGACGTCCGGATCCAGCCATGGCTGCCATCTGAAGGG
 AGTGATCACTTATCGGATAGGCGTTGCCCTGGGCTGCCCAAGGAGGACTAGAAGTCATTGCCA
 CTCAACCCCGCAGAGACCCTCTTCTTTGTGGACGAGTTTGACAACCTCATCATGATGTC
 CCCAGGATCATCCAGAACATTTGTACAGAGTTCAACTCACAGCCTCGGAAC**TGA**ATTACAG
 CAGGCAGACCCAGCAAGTGCTGCTTACTAAGTACGTGTTGGACCCACCCCGCTTAA
 TGGGACAGCAGCGGTGCATCAAGTCTTGGGCAGGGCATGGAGAAACAAATGTCTTGTATTA
 TTCTTTGCCATCATGCTTTTTCATATTCAAAACCTTGGAGTTGATCAAGATGATCAACAACGT
 ATAGAATGAGCCAAAGGGCTACATCATGTTGAGGTTGCTGGAGATTTTACATTTTGACAATT
 GTTTTCAAAATAAATGTTGGAATACAGTGCAGCCCTTACGACAGGCTTACGTAGAGCTTTT
 GTGAGATTTTTAAGTTGTTATTTCTGATTTGAACCTCTGTAACCCCTCAGCAAGTTTCAATTTT
 GTCATGACAATGTAGGAATTGCTGAATTAATGTTTGAAGGATGAAAAATGAAAAA
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 AA

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FIGURE 113

MRTVVLTMKASVIEMFLVLLVTVGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKC
PAGCQDPKYHVYGTVDYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSL
SLPRWRESFIVLESKPKKGVITYPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQPVVTLMQ
LLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSEQEMDLWSTATYTSSQNRPRADPGIQ
RQDPGAAAFQKPVGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFR
IQKQLLADVAQALDIGPAGPLMGVVQYGDNPATFNKTHTNRSRDLKTAIEKITQRGGLSNV
GRAISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAE
NEKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKTLPVLRVCDTDRACSKTCLNSADI
GFVIDGSSSVGTGNFRTVLQFVTNLTKFEISDSTDTRIGAVQYTYEQRLEFGFDKYSSKPD
LNAIKRVGYWGGTSTGAAINFALQLFKKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKG
VITYAIGVAWAAQEELEVIATHPARDHSFFVDEFNDLHQYVPRIIQNICTEFNSQPRN

CAGAGTGAACCTGGTTGCAGTGGCTGCTGCTGTGCGGGGGCGCTGAGAGGACACGAGCTCTA
TGCCCTTTCCGGCTGCTCATCCCGCTCGGCCTCTGTGCGCGCTGCTGCCTCAGCACCATTGGT
 GCGCCAGGTCCCGACGGCTCCGCGCCAGATCCCGCCACTACAGTTTTTCTCTGACTCTAAT
 TGATGCACTGGACACCTTGCTGATTTTTGGGAATGTCTCAGAATTCCAAAGAGTGGTTGAAG
 TGCTCCAGGACAGCGTGGACTTTGATATTGATGTGAACGCCTCTGTGTTTGAACAAACATT
 CGAGTGGTAGGAGGACTCTGTCTGCTCATCTGCTCTCCAAGAAGGCTGGGTGGAAGTAGA
 GGCTGGATGGCCCTGTTCCGGGCCTCTCTTGAGAATGGCTGAGGAGGCGGCCGAAAACCTCC
 TCCCAGCCTTTCAGACCCCACTGGCATGCCATATGGAACAGTGAACCTTACTTCATGGCGTG
 AACCAGGAGAGACCCCTGTCACTGTACGGCAGGGATTGGGACCTTCATTGTTGAATTTGC
 CACCCTGAGCAGCCTCACTGGTGACCCGGTGTTCCAAGATGTGGCCAGAGTGGCTTTGATGC
 GCCTCTGGGAGAGCCGGTCAGATATCGGGCTGGTCGGCAACCACATTGATGTGCTCACTGGC
 AAGTGGGTGCCCCAGGACGCAGGCATCGGGGCTGGCTGGACTCTACTTTAGTACTTTGG
 GAAAGGAGTGCCTGCTCTCAGGATAAGAAGCTCAGTGGCATGTTCCTAGAGATATAACAAG
 CACTCCGGAACATACACCCTTCGATGACTGGTACCTTGGGTTCAAGTGTACAAGGGGACT
 GTGTCCATGCCAGTCTTCCAGTCTTGGAGGCCACTGGCCTGGTCTTCAGAGCCTCATTGG
 AGACATTGACAATGCCATGAGGACCTTCTCAACTACTACACTGTATGGAAGCAGTTTGGGG
 GGCTCCCGGAATTCTACAACATTCCTCAGGGATACACAGTGGAGAAGCGAGAGGGCTACCCA
 CTTGCGCCAGAACTATTGAAAGCGCAATGTACCTCTACCGTGCCACGGGGGATCCCACCCT
 CCTAGAACTCGGAAGAGATGCTGTGGAATCCATTGAAAAATCAGCAAGGTGGAGTGGGAT
 TTGCAACAATCAAAGATCTGCGAGACCACAAGCTGGACAACCGCATGGAGTCGTTTCTCTG
 GCCGAGACTGTGAAATACCTCTACCTCCTGTTTGACCCAACCACTTCATCCACAACAATGG
 GTCCA^{CTT}TCGACGCGGTGATCACCCCTATGGGGAGTGCATCTGGGGGCTGGGGGGTACA
 TCTTCAACACAGAAGCTCACCCCATCGACCTTGCGGCCTGCACGTGCTGCCAGAGGCTGAAG
 GAAGAGCAGTGGGAGGTGGAGGACTTGATGAGGGAATTCTACTCTCTCAAACGGAGCAGGT
 GAAATTTCAGAAAAACACTGTTAGTTCCGGGCCATGGGAACCTCCAGCAAGGCCAGGAACAC
 TCTTCTCACCAGAAAAACATGACCAGGCAAGGGAGAGGAAGCCTGCCAAACAGAAGTCCCA
 CTCTCAGCTGACCCAGTCAACCTTACCTCCAAGTTGGCATTACTGGGACAGGTTTTCTCT
 AGGCTCCTCA**TGAC**CACTGGATAATTTTTTATTTTTATTTTTTTGAGGCTAACTATAATA
 AATTGCTTTTGGCCTATCATAAAA

FIGURE 115

MPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYFSLSLTLDALDTLLILGNVSEFQRVVE
VLQDSVDFDIDVNASVFETNIRVVGGLLSAHLSSKKAGVEVEAGWPCSGPELLRMAEEAARKL
LPAFQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSSLTGDPVFEDVARVALM
RLWESRSDIGLVGNHIDVLTGKWVAQDAGIGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNK
AIRNYTRFDDWYLVWQMYKGTVSMVPVFSLEAYWPGQLSLIGDIDNAMRTFLNYITVWKQFG
GLPEFYNIPOGYTVEKREGYPLRPELIESAMYLYRATGDPITLLELGRDAVESIEKISKVECG
FATIKDLRDHKLDRMESFFLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGY
IFNTEAHPIDLAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQKNTVSSGPWEPPARPGT
LFSPENHDQARERKPAKQKVPLLSCPSQPFTSKLALLGQVFLDSS

T0111"440660

FIGURE 116

AAAGTTACATTTTCTCTGGAACCTCTCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG
GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCTGGGCCGGCTCTAGAACAA
ATTACAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT
GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCA
AATGCAGACTTTTACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT
ACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCTC
TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCAGTGATCGCCCTGGAGA
AACAGTGTACTATTCTGTCGAATACAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT
GGATCCCCAGCAGCTGCTGCTCACTCACTGAAGTCTCTGAGTGTGATGTCACTGATGACATC
ACGGCCACTGTGCCATACAACCTTCGTGTGAGGGCCACATTGGGCTCACAGACCTCAGCCTG
GAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTACCCGACCTGGGATGGAGA
TCACCAAAGATGGCTTCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCGAGTTTGAGTTC
CTTGTTGGCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAATGGTGAGGATGG
GGGTATTCAGTGCACCTAGAAACCATGGAGCCAGGGGCTGCATCTGTGTAGGCGCCAGAG
CATTCGTGAAGGCCATTGGGAGGTGACCGCTTCAGCCAGACAGAATGTGTGGAGGTGCAA
GGAGAGGCCATTTCCCTGGTACTGGCCCTGTTTGCTTTGTTGGCTTCATGCTGATCCTTGT
TGCTGTGCCACTGTTGCTGTGAAATGGGCCGGCTGCTCCAGTACTCCTGTTGCCCGTGG
TGGTCTCTCCAGACACTTGAATAATACCACTTACCCCAGAAAGTTAATCAGCTGCAGAAAG
GAGGAGGTGGATGCTGTGCCACGGCTGTGATGTCTCCTGAGGAACCTCCTCAGGGCCTGGAT
CTCAT**TAG**GTTTGCGGAAGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAACCC
ATGAGGGGACAAGTTGTGTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA
GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACAC
TGACTGAGGCTTAGGGATGTGACCTCTAGACTGGGGGTGCCACTTGCTGGCTGAGCAACC
CTGGGAAAAGTGACTTCATCCCTTCGGTCTCTAAGTTTTCTCATCTGTAATGGGGGAATTACC
TACACACCTGCTAAACACACACACAGAGTCTCTCTATATATACACAGTACACATATAA
TACACCCAGCACTTGCAAGGCTAGAGGGAAACTGGTGACACTCTACAGTCTGACTGATTAG
TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT
GGCTTGAGAGAGCCACTTTCCCGAGAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG
TGTTGAGTTCACTTCAAGCCCAATGCCGGTGCAGAGGGGAATGGCTTAGCGAGCTCTACAGT
AGGTGACCTGGAGGAAGGTACAGCCACACTGAAAATGGGATGTGCATGAACACGGAGGATC
CATGAACTACTGTAAAGTGTGACAGTGTGTGCACACTGCAGACAGCGGTGAAATGTATGTG
GTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTGTTGTGTGCTCCTTTTTTC
TGTTGGTAAAGTACAGAATTACAGCAATAAAAAAGGGCCACCTTGGCCAAAAGCGGTAATAAA
AAAAA

FIGURE 117

MQTFTMVLEEIWTSLFMWFFYALIPCLLTDEVAILEPAPQNLSVLSTNMKLLMWSPVIAIGE
TVVYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECVTDITATVPYNLRVRATLGSQTS
SILKHPPFNSTILTRPGMEITKDGPHLVIELEDLGPQFEFLVAYWRREPAAEEHVKMVRSG
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPVLALFAFVGFMILIV
VVPLFVWKMGRLQLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

Important features:

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation sites.

amino acids 40-43 and 134-137

Tissue factor proteins homology.

amino acids 92-119

Integrins alpha chain protein homology.

amino acids 232-262

117/330 "117/330"

FIGURE 118

TCCTGCTGATGCACATCTGGGTTTGGCAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT
CCTGGCCGGCTCTAGAACATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC
CTGCCCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTCTGAATACCAGGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG
ATGTCACTGATGACATCAGGCCACTGTGCCATACAACCTTTGTGTGAGGGCCACATTGGGC
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCCTTAC
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG
GGCCCCAGTTTGAGTTCCTTGTGGCCTANTGGAGGAGGGGCGAACCCCTTGCGGCGCAAGGG
GTTNGCGAACCCCTTGCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCCAC
ATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

FIGURE 119

CGGACGCGTGGGCCGCCACCTCCGGAACAAGCCATGGTGGCGGCGACGGTGGCAGCGGCGTG
 GCTGCTCCTGTGGGCTGCGGCCTGCGCGCAGCAGGAGCAGGACTTCTACGACTTCAAGCGG
 TCAACATCCGGGGCAAACCTGGTGTGCTGGAGAAGTACCGCGGATCGGTGTCCCTGGTGGTG
 AATGTGGCCAGCGAGTGGGCTTCACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCG
 AGACCTGGGCCCCACCACCTTTAACGTGCTCGCCTTCCCCCTGCAACCAGTTTGGCCAACAGG
 AGCCTGACAGCAACAAGGAGATTGAGAGCTTTGCCCGCCGCACCTACAGTGTCTCATTCCCC
 ATGTTTAGCAAGATTGCAGTCACCGGTACTGGTGCCCATCCTGCCTTCAAGTACCTGGCCCA
 GACTTCTGGGAAGGAGCCACCTGGAACCTCTGGAAGTACCTAGTAGCCCCAGATGGAAAGG
 TGGTAGGGGCTTGGGACCCAACTGTGTCAGTGGAGGAGGTCAGACCCAGATCACAGCGCTC
 GTGAGGAAGCTCATCCTACTGAAGCGAGAAGACTTATTAACCACCGCGTCTCCTCCTCCACCA
 CCTCATCCGCCCCACCTGTGTGGGCTGACCAATGCAAACCTCAATGGTGTCTCAAAGGGAG
 AGACCCACTGACTCTCCTTCTCTTACTCTTATGCCATTGGTCCCATCATTCTTGTGGGGGAA
 AAATTCTAGTATTTTGATTATTTGAATCTTACAGCAACAATAGGAACCTCGGCCAATGAG
 AGCTCTTGACCAGTGAATCACCAGCCGATACGAACGCTCTTGCCAAACAAAAATGTGTGGCAA
 TAGAAGTATATCAAGCAATAATCTCCACCCAAAGGCTTCTGTAAACTGGGACCAATGATTAC
 CTCATAGGGCTGTTGTGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGC
 CAAATAGGAGGCATTCAATGAACATTTTTTGCATATAAACCAAAAAATAACTTGTTATCAAT
 AAAAAGTGCATCCAACATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTTAGTTGTT
 GTTATTTCTCTGTATTATTTTCTTCATTACAAAAGAAATGCAAGTTTATTGTAACAATCCA
 AACAATACCTCACGATATAAAATAAAATGAAAGTATCCTCCTCAAAA

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FIGURE 120

MVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGKLVSLVKYRGSVSLVVNVASECGFTDQ
HYRALQQLQRDLGPHHENVLAFFPCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTG
AHPAFKYLAQTSKGKPTWNFWKYLVPDGVVGAWDPTVSVEEVRPQITALVRKLILLKREDL

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FIGURE 121

CGGACGCGTGGGCGGGCCGGGACGCAAGCGAGCCATGGCTGTCTACGTCGGGATGC
 TGGCGCTGGGGAGGCTGTGCGCCGGGAGCTCGGGGGTGCTGGGGGCCGGGCCGCCCTCTCT
 CGGAGTTGGCAGGAAGCCAGGTTGCGAGGTTGCCGCTTCTCAGTTCCAGAGAGGTGGATCG
 CATGGTCTCCACGCCATCGGAGGCTCAGCTACGTTCAAGGGTGCACCAAAAGCATCTTA
 ACAGCAAGACTGTGGGCCAGTGCCTGGAGACCACAGCACAGAGGGTCCAGAACGAGAGGCC
 TTGGTCGTCTCCATGAAGACGTGAGTTGACCTTTGCCAACCAAGGAGGAGGTGGACAA
 AGCTGCTTCTGGCTCTCAGCATTTGGCTCTGCAAGGTGACCGGCTGGGCATGTGGGAC
 CTAATCCTATGCATGGTGCTCATGCAGTTGGCCACCGCCAGGCGGGCATCATTTCTGGTG
 TCTGTGAACCCAGCCTACCAGGCTATGGAAGTGGAGTATGTCTCAAGAAGGTGGGCTGCAA
 GGCCCTTGTGTTCCCCAAGCAATTCAGAGCCAGCAATACTACAACGCTCTGAAGCAGATCT
 GTCCAGAAGTGGAGAATGCCAGCCAGGGGCTTGAAGAGTCAGAGGCTCCAGATCTGACC
 ACAGTCATCTCGGTGGATGCCCTTTGCCGGGACCTGCTCCTGGATGAAGTGGTGGCGGC
 TGGCAGCACACGGCAGCATCTGGACCAGCTCCAATACAACAGCAGTTCTCTGCTGCCATG
 ACCCATCAACATCCAGTTCACTCGGGGACAAACGGCAGCCCCAAGGGGCCACCCCTCTCC
 CACTACAACATTGTCAACAACCTCAACATTTTAGGAGAGCGCTGAAACTGCATGAGAAGAC
 ACCAGAGCAGTTGCGGATGATCCTGCCAACCCCTGTACCATTGCCTGGGTTCCGTGGCAG
 GCACAATGATGTCTGTATGTACGGTGCCACCCTCATCTGGCCTCTCCCATCTTCAATTGGC
 AAGAAGGCACTGGAGGCCATCAGCAGAGAGAGAGGCACCTTCTGTATGGTACCCCCACGAT
 GTTCGTGGACATTCTGAACACGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAG
 GTGTCATTGCTGGGTCCCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAAT
 ATGAAGGACCTGGTGGTTGCTTATGGAACCACAGAGAACAGTCCCGTGACATTGCGCACTT
 CCTGAGGACACTGTGGAGCAGAAGGCAGAAAGCGTGGGCAGAAATATGCCTCACACGGAGG
 CCCGGATCATGAACATGGAGGCAGGGACGCTGGCAAAGCTGAACACGCCCCGGGGAGCTGTGC
 ATCCGAGGGTACTGCGTCATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGT
 GGATCAGGACAAGTGGTATTGGACAGGAGATGTGCCCAATGAATGAGCAGGGGCTTCTGCA
 AGATCGTGGGCCGCTCTAAGGATATGATCATCCGGGGTGGTGAGAACATCTACCCGCAGAG
 CTCGAGGACTTCTTTACACACACCCGAAGGTGCAGGAAGTGCAGGTGGTGGGAGTGAAGGA
 CGATCGATGGGGGAAGAGATTGTGCTGCATTGCGCTGAAGGACGGGAGGAGACACGG
 TGGAGGAGATAAAAGCTTCTGCAAAGGGAAGATCTCTCACTTCAAGATTCGGAAGTACATC
 GTGTTTGTCAACAACTACCCCTCACCATTTCAGGAAGATCCAGAAATTCAAACTTCGAGA
 GCAGATGGAACGACATCTAAATCTGTGAATAAAGCAGCAGGCCTGTCTGGCCGGTTGGCTT
 GACTCTCTCTGTGAGAAATGCAACCTGGCTTTATGCACCTAGATGTCCCCAGCACCCAGTTTC
 TGAGCCAGGCACATCAATGTCAAGGAATTGACTGAACGAACCTAAGAGCTCCTGGATGGGT
 CGGGAAGCTCGCTGGGACAAAGGTGCCAAAGGCAGGCAGCTGCCAGGCCCTCCCTCCTG
 TCCATCCCCACATTCCCTGTCTGTCTTGTGATTTGGCATAAAGAGCTTCTGTTTTCTTT
 GAAAAAAAAAAAAAAAAA

FIGURE 122

MAVYVGMRLRLGRLCAGSSGVLGARAALSRWQEARLQGVRFSSREVD RMVSTPIGGLSYVQ
 GCTKKHLNSKTVGQCLETTAQRVPEREALVVLHEDVRLTFAQLKEEVDKAASGLLSIGLCKG
 DRLGMWGPNSYAWVLMQLATAQAGIILVSVNPAYQAMELEYVLKKVGCKALVFPKQFKTQQY
 YNVLKQICPEVENAQPFGALKSQRLPDLTTVI SVDAPLP GTLLLDDEVVAAGSTRQHLDQLQYN
 QQFLSCHDPINIQFTSGTTGSPKGATLSHYNIVNNSNILGERLKLHEKTPEQLRMILPNPLY
 HCLGSVAGTMMCLMYGATLILASPIFNGKKALEAISRERGTFLYGTPTMFVDILNQPDFSSY
 DISTMCGGVIAGSPAPPELIRAI INKINMKDLVVAYGTENSVPVTF AHFPEDTVEQKAESVG
 RIMPHTEARIMNMEAGTLAKLNTPGELCIRGYCVMLGYWGEPQKTEEAVDQDKWYWTGDVAT
 MNEQGFCIKIVGRSKDMIIRGENIYPAELEDDFFHTHPKVQEVQVVGVKDDRMGEEICACIRL
 KDGEETTVEEIKAFCKGKISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL

Signal Peptide:

amino acids 1-22

Transmembrane Domains:

amino acids 140-161, 213-229, 312-334

Putative AMP-binding Domain Signature:

amino acids 260-271

N-myristoylation Sites:

amino acids 19-24, 22-27, 120-125, 203-208, 268-273, 272-277,
 314-319, 318-323, 379-384, 380-385, 409-413

N-glycosylation Site:

amino acids 282-285

FIGURE 123

CAACTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGACACCAGAGCAGTTGCGGA
TGATCCTGCCAACCCTGTACCATTCGCTGGGTTCCGTGGCAGGCACAATGATGTGTCTG
ATGTACGGTGCCACCTCATCCTGGCCTCTCCCATCTTCAATGGCAAGAAGGCACTGGAGGC
CATCAGCAGAGAGAGAGGCACCTTCCTGTATGGTACCCCCACGATGTTCTGTGGACATTCTGA
ACCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAGGTGTCATTGCTGGGTCC
CCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAATATGAAGGACCTGGTGGT
TGCTTATGGAACCACAGAGAACAGTCCCGTGACATTCGCGCACTTCCCTGAGGACACTGTGG
AGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGGCGCGGATCATGAACATG
GAGGCAGGGACGCTGGCAAAGCTGAACACGCCCGGGGAGCTGTGCATCCGAGGGTACTGCGT
CATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGGATCAGGACAAGTGGT
ATTGGACAGGAGATGTCGCCAC

FIGURE 124

GAGCAGGACGGAGGCC**ATG**ACCCCGCCAGGAAAGCAGGTGCCAGGCCATGATCTGGACTGC
 AGGCTGGCTGCTGCTGCTGCTTCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCG
 TGCAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGC GC CGCGGGC
 GTGGACGTCTGCACCGAGGCCGTGGGGGCGGTGGAGACCATCCACGGACAATTCTCGTGGC
 AGTGC GG GGT T T GCGGTTCGGGACTCCCCGGCAAGAATGACCGCGGCCTGGATCTTCAGGGGC
 TTCTGGCGTTTATCCAGCTGCAGCAATGCGCTCAGGATCGCTGCAACGCCAAGCTCAACCTC
 ACCTCGCGGGGCGCTCGACCCGGCAGGTAATGAGAGTGATACCCGCCAACGGCGTGGAGTG
 CTACAGCTGTGTGGGCTGAGCCGGGAGGCGTGCCAGGGTACATCGCCGCCGTGCTGAGCT
 GCTACAACGCCAGCGATCATGTCTACAAGGGCTGCTTCGACGGCAACGTCACCTTGACGGCA
 GCTAATGTGACTGTGTCTTGCTGTCCGGGGCTGTGTCCAGGATGAATTCTGCATCGGGA
 TGGAGTAACAGGCCAGGGTTCACGCTCAGTGGCTCCTGTTGCCAGGGGTCCCGCTGTAAC
 CTGACCTCCGCAACAAGACCTACTTCTCCCTCGAATCCCAACCCCTTGTCGGCTGCCCCCT
 CCAGAGCCACGACTGTGGCTCAACCACATCTGTCAACACTTCTACCTCGGCCCCAGTGAG
 ACCACATCCACCACCAAAACCATGCCAGCGCCAACAGTCAGACTCCGAGACAGGGAGTAG
 AACACGAGGCCTCCCGGGATGAGGAGCCAGGTTGACTGGAGGCGCGCTGGCCACCAGGAC
 CGCAGCAATTCAGGGCAGTATCCTGCAAAAGGGGGCCCCAGCAGCCCATATAAAGGCTG
 TGTGGCTCCACAGCTGGATTGGCAGCCCTTCTGTTGGCCGTGGCTGCTGGTGTCTACTG**T**
GAGCTTCTCCACCTGGAAATTTCCCTCTCACCTACTTCTCTGGCCCTGGGTACCCCTCTTCT
 CATACTTCTGTTCACCACCTGGACTGGGCTGGCCAGCCCTGTTTTTCCAACATTCCC
 CAGTATCCCCAGCTTCTGTGTGCGTGGTTTGGCGCTTTGGGAATAAAATACCGTTGTATAT
 ATTCTGCCAGGGGTGTTCTAGCTTTTTGAGGACAGCTCCTGTATCCTTCTCATCCTTGTCTC
 TCCGCTTGTCTCTTGTGATGTTAGGACAGAGTGAGAGAAGTCAGCTGTACGGGGAAGGTG
 AGAGAGAGGATGCTAAGCTTCTACTCACTTTCTCCTAGCCAGCTGGACTTTGGAGCGTGG
 GGTGGGTGGGACAATGGCTCCCCACTCTAAGCACTGCCTCCCTACTCCCGCATCTTTGGG
 GAATCGGTTCCCATATGTCTTCTTACTAGACTGTGAGCTCCTCGAGGGGGGCGCGGTAC
 CCAATTCGCCCTATAGTGAGTCGA

FIGURE 125

MDPARKAGAQAMIWTAGWLLLLLLRGGAQALECYSCVQKADDGCSFNKMKTVKCAPGVDVCT
EAVGAVETIHGQFSLAVRGCGSGLPGKNDRGLDLHGLLAFIQLQQCAQDRCNALNLTSRAL
DPAGNESAYPPNGVECYSCVGLSREACQGTSPPVVSCYNASDHVYKGCDFGNVTLTAANVTV
SLPVRGCVQDEFCTRDTVGPFTLSGSCCQGSRCNSDLRNKTYFSPRIPPLVRLPPPEPTT
VASTTSVTTSTSAPVRPTSTTKMPAPTSQTPRQGEHEASRDEEPRLTGGAAGHQDRSNSG
QYPAKGGPQQPHNKGCVAPTAGLAALLAVAAGVLL

FDATT"4440660

[illegible]

FIGURE 127

MELVLVFLCSLLAPMVLASAAEKEKEMDPFHYYDQTLRIGGLVFAVVLFSVGILLILSRCK
CSFNQKPRAPGDDEEAQVENLITANATEPQKQRTVEVQPSGSLWNLRLLLEPLDANVDA

WILLIAM L. HARRIS

FIGURE 128

AAACTTGACGCCATGAAGATCCCGGTCCTTCCTGCCGTGGTGCTCCTCTCCCTCCTGGTGCT
CCACTCTGCCCAGGGAGCCACCCTGGGTGGTCCTGAGGAAGAAAAGCACCATTGAGAATTATG
CGTCACGACCCGAGGCCCTTTAACACCCCGTTCCTGAACATCGACAAATTGCGATCTGCGTTT
AAGGCTGATGAGTTCCTGAACTGGCACGCCCTCTTTGAGTCTATCAAAGGAAACTTCCTTT
CCTCAACTGGGATGCCTTTCCTAAGCTGAAAGGACTGAGGAGCGCAACTCCTGATGCCCAGT
GACCATGACCTCCACTGGAAGAGGGGGCTAGCGTGAGCGCTGATTCTCAACCTACCATAACT
CTTTCCTGCCTCAGGAACTCCAATAAACATTTCCATCCAAA

TCTTCTGCTCAGGAACTCCAATAAACATTTCCATCCAAA

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FIGURE 129

MKIPVLPAVVLLSLLVLHSAQGATLGGPEEESTIENYASRPEAFNTPFLNIDKLRSFAKDE
FLNWHALFESIKRKLPFLNWDAFPKLKGLRSATPDAQ

TO THE EDITOR

FIGURE 130

CAGTTCTGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCCATGGGGGTGGAGATTGC
CTTTGCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCAGGTTGTTTC
TTCTCCAGCCAGTTCCAACCTCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCCTGTGGC
TTTGCCGGCCACTCATGAGAGTGTTTTTTGTGTAAAGTATTTTTTAGAATACTGTTGACTTCT
TCATGATTTAATAACCATCCTTTGCGAAGTTTTATGAGGCTTTAGGGGAATGTCAACCCCTCA
AATTTTTGTTATACTAGATGGCTTCCATTTACCCACCACTATTTTAAGGTCCCTTTATTTTT
AGGTTCAAGGTTCAATTTGACTTGAGAAAGTGCCCTTCTGCAGCTTCATTGATTTTGTTTATC
TTCATAATTAATTGTAACGATTAAAAAGAATAAGAGCACGCAGACCTCTAGGAGAATATTT
TATCCCTGGGTGCCCCCTGACACATTTATGTAGTGATCCACAAATGTGATTGTTAATTTAAA
TGTTATTCTAATATTAGTACATTAGTTGTGATGTAATATGAATAACCAGAATCTATTTCTT
AAAAGTTTTGAGTATATTTTCACTAGATATTTGTATAGAAAGACTGAATAGTGATG

FIGURE 131

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FIGURE 132

GGGGAATCTGCGAGTAGGTCTGCCGGCG**ATG**GAGTGGTGGGCTAGCTCGCCGCTTCGGCTCTG
 GCTGCTGTTGTTCTCTCTGCCCTCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAATGGA
 AAGTATTTATTGACCAAAATTAACAGGTC'TTTGGAGAATTACGAACCATGTTCAAGTCAAAC
 TGCAGCTGCTACCATGGTGTATAGAAAGAGGATCTAACTCCTTTCCGAGGAGGCATCTCCAG
 GAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATCACTAAGAACA
 GACTGTACCGGGGAAAATGACTGCATGTTCCCTCAAGGTGTAGTGGTGTGAGCAC'TTTATT
 TTGGAAGTGATCGGGCGTCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCCTCA
 GGTTCCTAAATGGATGGAGCCTGCCATCCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACC
 ATGATATCATGTATCCTGCTTGGACATTTTGGGAAGGGGGACCTGCTGTTTGGCCAATTTAT
 CCTACAGGTCTTGGACGGTGGGACCTCTTCAGAGAAGATCTGGTAAGGTCAGCAGCACAGTG
 GCCATGGA AAAAGAAAACTCTACAGCATATTTCCGAGGATCAAGGACAAGTCCAGAACGAG
 ATCCTCTCATCTCTGTCTCGGAAAAACCCAAAAC'TGTTGATGCAGAAATACACCAAAAAC
 CAGGCCTGGAATCTATGAAAGATACCTTAGGAAAGCCAGCTGCTAAGGATGTCCATCTTGT
 GGATCACTGCAAAATACAAGTATCTGTTTAATTTTCGAGGCGTAGCTGCAAGTTTCCGGTTTA
 AACACCTCTTCTGTGTGGCTCACTGTGTTTCCATGTGGTGATGAGTGGCTAGAATTCTTC
 TATCCACAGCTGAAGCCATGGGTTCACTATATCCAGTCAAAACAGATCTCTCCAATGTCCA
 AGAGCTGTTACAATTTGTAAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAAAGGGGAA
 GCCAGTTTATTAGGAACCATTTGCAGATGGATGACATCACCTGTTACTGGGAGAACCTCTTG
 AGTGAATACTCTAAATTCCTGTCTTATAATGTAACGAGAAGGAAAGGTTATGATCAAATTAT
 TCCCAAAATGTTGAAAACGAAC**TAG**TAGTCATCATAGGACCATAGTCTCTTTGTGGCA
 ACAGATCTCAGATATCCTACGGTGAGAAGCTTACCATAAGCTTGGCTCCTATACCTTGAATA
 TCTGCTATCAAGCCAAATACCTGGTTTTCTTATCATGCTGCACCCAGAGCAACTCTTGAGA
 AAGATTTAAATGTGTCTAATACACTGATATGAAGCAGTTCAACTTTTGGATGAATAAGGA
 CCAGAAATCGTGAGATGTGGATTTTGAACCAACTCTACCTTTCATTTTCTTAAGACCAATC
 ACAGCTTGTGCCTCAGATCATCCACCTGTGTGAGTCCATCAGTGAATTTGACTGTGTCCA
 TGTGATGATGCCCTTTGTCCCATTATTGGAGCAGAAAAATTCGTCAATTTGGAAGTAGTACAA
 CTCATTGCTGGAATTTGTGAAATATTCAAGGCGTGATCTCTGTCACTTTATTTTAATGTAGG
 AAACCCATATGGGGTTTATGAAAATACTTGGGGATCATTCTCTGAATGGTCTAAGGAAGCGG
 TAGCCATGCCATGCAATGATGTAGGAGTTCTCTTTGTAAAACCATAAATCTGTACTCAG
 GAGGTTTCTATAATGCCACATAGAAAGAGGCCAATTGCATGAGTAATATTGCAATTGGATT
 TCAGGTTCCCTTTTGTGCCTTCATGCCCTACTTCTTAATGCCTCTCTAAAGCCAAA

GGGGAATCTGCGAGTAGGTCTGCCGGCGATGAGTGGTGGGCTAGCTCGCCGCTTCGGCTCTG

MEWWASSPLRLWLLFLFLPSAQGRQKESGSKWKVFDIQINRSLENYEPCCSSQNCSCYHGVE
EDLTPFRGGISRKMMAEVVRRLGLTHYQITKNRLYRENDCMFPRSCEVHEHFILEVIGRLPD
MEMVINVRDYPQVPKMWEPAPVFSFSKTEYHDIIMYPAWTFWEGGPAVWPIYPTGLGRWDL
FREDLVRSAAQWPWKKNSTAYFRGSRTPERDPLILLSRKNPKLVDAEYTKNQAWKSMKDT
LGKPAAKDVHLDHCKYKYLNFNFRGVAASFRFKHLFLCGSLVFHVGDWLEFFYPQLKPWVH
YIPVKTDLNSNVQELLQFVKKANDDDVAQEIAERGSQFIRNHLQMDITCYVENLLSEYSKFLSY
NDDRKGYDQIIEPKMLKTEL

FIGURE 134

CACCCCTCCATTCTCGCCATGCCCCCTGCACTGCTCCTGATCCCTGCTGCCCTCGCCTCTT
 TCATCCTGGCCTTTGGCACCGGAGTGGAGTTGCTGGCCTTTACCTCCCTTCGCCCACTTCTT
 GGAGGGATCCCGAGTCTGGTGGTCCGGATGCCCGCCAGGATGGCTGGCTGCCCTGCAGGA
 CCGCAGCATCCTTGCCCCCTGGCATGGGATCTGGGGCTCCTGCTTCTATTGTGGGCAGC
 ACAGCCTCATGGCAGCTGAAAGAGTGAAGGCATGGACATCCCGGTACTTTGGGGTCTTTCAG
 AGGTCACTGTATGTGGCTGCACTGCCCTGGCCTTGACGTGGTGATGCGGTACTGGGAGCC
 CATACCCAAAGGCCCTGTGTTGTGGGAGGCTCGGGCTGAGCCATGGGCCACCTGGGTGCCGC
 TCCTCTGCTTTGTGCTCCATGTATCTCCTGGCTCCTCATCTTTAGCATCCTTCTCGTCTTT
 GACTATGCTGAGCTCATGGGCCTCAAACAGGTATACTACCATGTGCTGGGGCTGGGCAGCC
 TCTGGCCCTGAAGTCTCCCCGGGCTCTCAGACTCTTCTCCCACCTGCGCCACCCAGTGTGTG
 TGGAGCTGCTGACAGTGTGTGGTGGTGCTACCTGGGCACGGACCGTCTCCTCCTTGCT
 TTCTCTCTTACCCTCTACCTGGGCCTGGCTCACGGGCTTGATCAGCAAGACCTCCGCCTACCT
 CCGGGCCAGCTACAAAGAAAACCTCCACCTGCTCTCTCGGCCCAAGGATGGGGAGGCAGAGT
GAGGAGCTCACTCTGGTTACAAGCCCTGTTCTTCTCTCTCCCACTGAATTCTAAATCCTTAAC
 ATCCAGGCCCTGGCTGCTTCATGCCAGAGGCCCAAATCCATGGACTGAAGGAGATGCCCTT
 CTACTACTTGAGACTTTATTCTCTGGGTCCAGCTCCATACCCTAAATCTGAGTTTCAGCCA
 CTGAACCTCAAGGTCCACTTCTCACCAGCAAGGAAGAGTGGGGTATGGAAGTCATCTGTCCC
 TTCACTGTTTAGAGCATGACACTCTCCCCCTCAACAGCCTCCTGAGAAGGAAAGGATCTGCC
 CTGACCACTCCCCTGCCACTGTTACTTGCCCTCTGCGCCTCAGGGGTCCCCTTCTGCACCGCT
 GGCTTCCACTCCAAGAAGGTGGACCAGGGTCTGCAAGTTC AACGGTCATAGCTGTCCCTCCA
 GGCCCCAACCTTGCTCACCCTCCCGGCCCTAGTCTCTGCACCTCCTTAGGCCCTGCCTCT
 GGGCTCAGACCCCAACCTAGTCAAGGGGATTCTCCTGCTCTTAACTCGATGACTTGGGGCTC
 CCTGCTCTCCCGAGGAAGATGCTCTGCAGGAAAATAAAAGTCAGCCTTTTTCTAAAAAAA

FIGURE 135

MAPALLLI PAALASFILAFGTGVEFVRFTSLRPLLGGIPESGGPDARQGWLAAALQDRSILAP
LAWDLGLLLLLFVGQHSLSMAAERVKAWTSRYFGVLQRSLYVACTALALQLVMRYWEPIPKGPV
LWEARAEPWATWVPLLCFVLHVVISWLLIFSILLVFDYAELMGLKQVYYHVLGLGEPLALKSP
RALRLFSLRHPVCVELLTVLWVPTLGTDRLLLAFLLTLYLGLAHLDDQDLRYLRAQLQR
KLHLLSRPQDGEAE

Signal sequence:

amino acids 1-13

Transmembrane domains:

amino acids 58-76, 99-113, 141-159, 203-222

N-myristoylation sites:

amino acids 37-43, 42-48, 229-235

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FIGURE 136

CCGAGCACAGGAGATTGCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGA
 AGAAATTGCCAAACCATGTCTTTTTTCTGTTTTTCAGAGTAGTTCACAAACAGATCTGAGTGT
 TTTAATTAAGCATGGAATACAGAAAACAACAAAAAAGCTTAAGCTTTAATTTTCATCTGGAATT
 CCACAGTTTTCTTAGCTCCCTGGACCCGGTTGACCTGTTGGCTCTTCCCGCTGGCTGCTCTA
 TCACGTGGTGTCTCCGACTACTCACCCGAGGTAAAGAACCCTTCGGCTCGCGTGCTTCTG
 AGCTGCTGTGGATGCGCTCGGCTCTCTGGACTGTCTTCCGAGTAGGATGTCACTGAGATCC
 CTCAATGGAGCCTCCTGCTGCTGTCACTCCTGAGTTTCTTTGTGATGTGGTACCTCAGCCT
 TCCCCACTACAATGTGATAGAACGCGTGAAGTGGATGTACTTCTATGAGTATGAGCCGATTT
 ACAGACAAGACTTTCACTTCACACTTCGAGAGCATTCAAAGTGTCTCATCAAAATCCATTT
 CTGGTCATTCTGGTGACCTCCCACCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTAC
 TTGGGGTGAAAAAAGTCTTGGTGGGATATGAGGTTCTTACATTTTTCTTATTAGGCCAAG
 AGGCTGAAAAGGAAGACAAAATGTTGGCATTGTCTTAGAGGATGAACACCTTCTTTATGGT
 GACATAATCCGACAAGATTTTTTAGACACATATAATAACCTGACCTTGAAAACCATTATGGC
 ATTCAGGTGGTAAGTGAAGTTTGGCCCAATGCCAAGTACGTAATGAAGACAGACACTGATG
 TTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTAAACCTAAACCACTCAGAGAAGTTT
 TTCACAGGTTATCCTCTAATTGATAATTATTCCTATAGAGGATTTTACCAAAAAACCATAT
 TTCTTACCAGGAGTATCCTTTCAAGGTGTTCCCTCCATACTGCAGTGGGTGGGTTATATAA
 TGTCAGAGATTTGGTGGCAAGGATCTATGAAATGATGGGTCAAGTAAACCCATCAAGTTT
 CAAGATGTTTATGTCGGGATCTGTTTGAATTTATTAAGTGAACATTTCATATTCCAGAAGA
 CCAAAATCTTTTCTTTCTATATAGAATCCATTTGGATGTCTGTCAACTGAGACGTGTGATTG
 CAGCCCATGGCTTTTCTTCAAGGAGATCATCACTTTTTTGGCAGGTGCTGCTAAGGAACACC
 ACATGCCATTATTAAGCTTCACATTCTACAAAAAGCCTAGAAGGACAGGATACCTTGTGAAA
 GTGTTAAATAAAGTAGGTACTGTGAAAATTTCATGGGAGGTGAGTGTGCTGGCTTCACTG
 AACTGAAACTCATGAAAAACCCAGACTGGAGACTGGAGGGTTACACTGTGATTATTAGTC
 AGGCCCTTCAAAGATGATATGTGGAGGAATTAATATAAAGGAATGGAGGTTTTTGTGCTAA
 GAAATTAATAGGACCAACAATTTGGACATGTCATTCTGTAGACTAGAATTTCTTAAAGGG
 TGTTACTGAGTTATAAGCTCACTAGGCTGTAAAAACAAACAATGTAGAGTTTTATTATTG
 AACATGTAGTCACTTGAAGGTTTTGTGTATATCTTATGTGGATTACCAATTTAAAAATATA
 TGTAGTTCTGTGTCAAAAACTTCTTCACTGAAGTTATACTGAACAAAATTTTACCTGTTTT
 TGGTCATTTATAAGTACTTCAAGATGTTGCAGTATTCACAGTTATTATTATTTAAATTA
 CTTCAACTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAGGATAGTGAAT
 CATTCTTTACATGCAACATTTTCCAGTTACTTAACTGATCAGTTTATTATTGATACATCAC
 TCCATTAATGTAAGTCATAGGTCATTATTGCATATCAGTAATCTCTTGGACTTTGTTAAAT
 ATTTTACTGTGGTAATATAGAGAAGAATTAAAGCAAGAAAATCTGAAA

FIGURE 137

MASALWTVLPSRMSLRSLKWSLLLLSLSSFVMWYLSLPHYNVIERVNWMYFYEYEPYRQD
FHFTRLREHSNCSHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEAEK
EDKMLALSLEDEHLLYGDIRQDFLDTYNNLTLTIMAFRWVTEFCPNAKYVMKTDTDVFIN
TGNLVKYLNLNLHSEKFFTGYPIDNYSYRGFYQKTHISYQEYFPKVFPPYCSGLGYIMSRD
LVPRIYEMMGHVKPIKFEDVYVGICLNLKVINIHIPEDTNLFFLYRIHLDVCQLRRVIAAHG
FSSKEIITFWQVMLRNTTCHY

[illegible]

FIGURE 138

CCTCTGTCCACTGCTTTCTGTAAGACAAGATGAAGTTCACAATTGTCTTTGCTGGACTTCTT
GGAGTCTTTCTAGCTCCTGCCCTAGCTAACTATAATATCAACGTCAATGATGACAACAACAA
TGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAATGAACACAATGTGGCCAATGTTGACA
ATAACAACGGATGGGACTCCTGGAATTCCATCTGGGATTATGGAATGGCTTTGCTGCAACC
AGACTCTTTCAAAAGAAGACATGCATTGTGCACAAAAATGAACAAGGAAGTCATGCCCTCCAT
TCAATCCCTTGATGCACTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGACCAGGAGGACCAC
CTCCAAGGGCCTGATGTACTCAGTCAACCCAAACAAAGTCGATGACCTGAGCAAGTTCGGA
AAAAACATTGCAACATGTGTCTGGGATTCCAACATACATGGCTGAGGAGATGCAAGAGGC
AAGCCTGTTTTTTTACTCAGGAACGTGCTACACGACCAGTGACTATGGATTGTGGACATTT
CCTTCTGTGGAGACACGTTGGAGAACTAAACAATTTTTTAAAGCCACTATGGATTTAGTCAT
CTGAATATGCTGTGCAGAAAAAATATGGGCTCCAGTGGTTTTTACCATGTCATTCTGAAATT
TTTCTCTACTAGTTATGTTTGATTCTTTAAGTTTCAATAAAATCATTTAGCATTGAAAAAAA

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FIGURE 139

MKFTIVFAGLLGVFLAPALANYNINVNDDNNNAGSGQQSVSVNNEHNVANVDNNGWDSWNS
IWDYGNNGFAATRLFQKKTCIVHKMNKEVMPISIQSLDALVKEKKLQGKGPGGPPKGLMYSVN
PNKVDDLKFKGNIANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCGDTVEN

Signal Peptide:

amino acids 1-20

N-myristoylation Sites:

amino acids 67-72, 118-123, 163-168

Flavodoxin protein homology:

amino acids 156-174

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FIGURE 140

CATTCTGAAACTAATCGTGTGCAGAAATTGACTTTGAAAAGCATTGCTTTTTACAGAAGTATA
TTAACTTTTTAGGAGTAATTTCTAGTTTGGATTGTAATATGAAATAATTTAAAAGGGCTTCG
CTCATATATAGGAAAAATCGCATATGGTCTAGTATTAATTTCTTATTGCTTACTGATTTTTT
TGAGTTAAGAGTTGTTATATGCTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAA
GAATAAAGTAGATTGAGTCTCCAATTTTATGTAAAGCTTCAGAAGAAGCTGGTTTGTTACATG
CAAGCTTATAGTTGAAATATTTTTTCAGGAATTACATGAATGCAGCTCTCGAACCAATGTGT
TTGTTTCGATTTCAACCAGAGACTATAGCATGTGCTTGCATCTACCTTGCAGCTAGAGCACTT
CAGATTCGGTGGCAACTCGTCCCATTTGGTTTCTTCTTTTTGGTACTACAGAAGAGGAAAT
CCAGGAAATCTGCATAGAAACACTTAGGCTTTATACAGAAAAAGCCAAACTATGAATTAC
TGGAAAAAGAAGTAGAAAAAGAAAAAGTAGCCCTTACAAGAAGCCAAATTTAAAGCAAAGGGA
TTGAATCCGGATGGAACCTCAGCCCTTTCAACCTCGGGTGGATTTCTCCAGCTCCCAAGCC
ATCATCACCAGAGAAGATTAAGAGCTGAAGAGAATAACCAATTCTCCATTATGTGAAGACAG
TGACAAAAAGAACTGAGGATAGACACAGGCTTCCAAGGCCCTTACAAATGGTGTAAAGAAA
GACAGAAAGAGAAGTAGAAATAGCAGAAGTGCAGAGTCGATCGAGGTCAAGAACACGCATCAG
TCTAGATCACATACTCCAAGAAGACACTATAATAATAGGCGGAGTCGATCTGGAACATACA
GCTCGAGATCAAGAAGCAGGTCCCGCAGTCACAGTGAAGGCCCTCGAAGACATCATAATCAT
GGTTCCTCTCACCTTAAGGCCAAGCATACCAGAGATGATTTAAAAAGTTCAAACAGACATGG
TCATAAAAGGAAAAAATCTGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAG
CCAAGAAACACAGGCATGAAAGGGACATCATAGGGACAGGCGTGAACGATCTCGCTCCTTT
GAGAGGTCCCATAAAGCAAGACCATGGTGGCAGTCGCTCAGGACATGGCAGGCACAGGCG
CTGACTTTCTCTTCCCTTTGAGCCTGCATCAGTTCTTGTTTTGCCTATCTACAGTGTGATGT
ATGGACTCAATCAAAACATTAAACGCAAACCTGATTAGGATTTGATTTCTTGAAACCCCTCA
GGTCTCTAGAACACTGAGGACAGTTTCTTTTGAAAAGAACTATGTTAATTTTTTTGCACATT
AAAATGCCCTAGCAGTATCTAATTA AAAACCATGGTCAGGTTCAATTGTACTTTATTATAGT
TGTGTATTGTTTATTGCTATAAGAAGACTGGAGCTGAATCTGTAAAAATGTATCTTATTTT
ATACAGATAAAATTGCAGACACTGTTCTGATTTTAAGTGGTTATTGTGTTAAATGATGGTGAAT
ACTTTCTTAACACTGGTTTGTCTGCATGTGTAAAGATTTTACAAGGAAATAAAATACAAAT
CTGTTTTTTTTCTAAAAA AAAAAAAAAAAAAAAGT

FIGURE 141

MNDLSRTNVFVRFPETIACACIYLAARALQIPLPTRPHWFLFGTTEEEIQEICIETLRLY
TRKKPNYELLEKEVEKRRKVALQEAKLKAKGLNPDGTPALSTLGGFSPASKPSSPREVKAEK
SPISINVKTVKKFEDRQQAQSPYNGVRKDSKRKSRSASRSASRSRTRSSRSRSHTPRRHY
NRRSRSGTYSRRSRSRSHSPYRRHHNHGSPHLKAKRTRDDLKSRNRHGHRKKRSRSRSQ
SKSRDSDAAKKHRHRRGHHRRDRRSRSRSPERSHKSHKHGGSRSGHGRHR

FIGURE 142

TGGGGATAAAGGAAAAATGGTCAGGTATTAAATGGCTTAAAGATTATTGGAAGGGGTTTATCA
TTTTTTGAANNATTTCGGGTCANAATTGNCTTTGAAAAGCATTGCTTTTTACAGAAATATAT
TANCTTTTtagagTAaTTTCTagTTTGaTTGTaATATGAaATTATTTAAaAGGGCTTCGCT
CATATATAGGAAAATCGCATATGGTCCTAGTATTAAATTNTTATTGCTTACTGATTTTTTTG
AGTTAAGAGTTGTTATATGNTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAGA
ATAAAGTAGATTGAGTCTCCAATTTTATGTAAAGCTTCAGAAGAACTGGTTTGTTTACATGCA
AGCTTATAGTTGAAATATTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGTTT
GTTTCGATTTCAACCAGAGANTATAGCATGTGCTTGCACTACCTTCAGNNTAGAGCAATTA
GATTCCGTTGCCAACTNGTCCCCATTGGTTTTCTCTTTTTTGGTACTACAGAAGAGCAATTC
AGGAAATNTGCATAGAAACACTTAGGCTTTTATACCGAAAAAGCCAAACTATGAATTACTG
GAAAAAGAAAGTAGAAAAAAGAAAGTAGCCTTACAAGAAAGCCNAATTAAAGCAaAGGGATT
GAATCCGGATGGAaCTCCAGCCCTTTCAACCCTGGGTGGATTTTCTCC

GGACACGAGGCCTCGTGCCAAAGCTTGGCACGAGGGTGCACCGCGTTCTCGCACCGCTCA**ATG**CG
GGTCTCTCGGAGTACAGCTGGTGGTGACCTGCTCACTGCCACCCTCATGCACAGGCTGGCGC
CACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAACCGCAGTTTGTTCGGATACAAGCACCCG
TCTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCCAGAGGCAGGAAAGAGCGGTG
GGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCCGAGATGCCCCGTTCCAGCTGG
AGACCTGCCCTTCACGACCGTGGATGCCCTGGTCTCGCGCTTCTTCTCGAGTACCAAGTGG
TTTGTGGACTTTGCTGTGTACTCGGGCGCGTGTACCTCTTCACAGAGGCCTACTACTACAT
GCTGGGACAGCCAAGGAGACTAACATTGCTGTGTTCTGGTGCTCTACGGTGACCTTCT
CCATCAAGATGTTCTGACAGTGACACGGCTGTACTTCAGCGCCGAGGAGGGGGGTGAGCGC
TCTGTCTGCCTCACCTTTGCTTCTCTTCTCTGCTGCTGGCCATGCTGGTGCAAGTGGTGCG
GGAGGAGACCCCTCGAGCTGGGCCTGGAGCCTGGTCTGGCCAGCATGACCCAGAACTTAGAGC
CACTTCTGAAGAAGCAGGGCTGGGACTGGGCGCTTCTCGTGCCAAAGCTGGCTATCCGCGTG
GGACTGGCAGTGGTGGGCTCTGTGCTGGGTGCTTCTCACTTCCCTCCAGGCGTGGCGGTGCG
CCAGACCCACCGGGAGCGCACTGACCATGTGCGAGGACAGACCCATGCTGCAGTTCTCTCTGC
ACACAGCTTCTCTGCTCCCCGTTCATCCTGTGGCTCTGGACAAAGCCCATTGCACGGGA
TTCCTGCACACGCGCGCTTTGGGGAGACGCGTTTCTCCCTGCTGTCCGATTCTGCCTTCGA
CTCTGGGCGCTCTGGTTGCTGGTGGTGCTGTGCCTGCTGCGGCTGGCGGTGACCCGGCCCC
ACCTGCAGGCCTACCTGTGCTGGCCAAGGCCCGGGTGGAGCAGTGCGAAGGGAGGCTGGC
CGCATCGAAGCCCGTGAATCCAGCAGAGGGTGGTCCGAGTCTACTGCTATGTGACCGTGGT
GAGCTTGAGTACCTGACGCCGCTCATCTCACCTCAACTGCACACTTCTGCTCAAGACGC
TGGGAGGCTATTCTCGGGCCTGGGCCAGTCTCTTACTATCCCCGACCCATCCTCAGCC
AGCGCTGCCCCCATCGGCTCTGGGGAGGACGAAGTCCAGCAGACTGCAGCGCGGATTGCCGG
GGCCCTGGGTGGCCTGCTTACTCCCCCTTCTCCTCCGTGGCGTCTGGCCTACCTCATCTGGT
GGACGGCTGCCTGCCAGCTGCTGCCAGCCCTTTTCGGCTCTACTTCCACCAGCACTTGGCA
GGCTCT**TAG**CGCTGCCTGCAGACCTTCTGGGGCCCTGAGGTCTGTTCTGGGGCAGCGGACA
CTAGCCTGCCCCCTCTGTTTTCGCCCCCGTGTCACAGCTGCAAGGTGGGCGGACTCCCC
GGCGTTCCTTCCACCACAGTGCTGACCCGCGGCCCCCTTGAGCGCCGAGTTTCTGCTCA
GAACTGTCTCTCTGGGCCAGCAGCATGAGGGTCCCGAGGCCATTGTCTCGGAAGCGTATG
TGCCAGGTTTGAGTGGCAGGGTGATGCTGGCTGCTTCTTGAACAAATAAAGGAGCATGCC
GATTTTAA

FIGURE 144

MAVLGVQLVVTLLTATLMHRLAPHCSFARWLLCNGSLFRYKHPSEEEELRALAGKPRPRGRKE
RWANGLSEEKPLSVPRDAPFQLETCPLTTVDALVLRFFLEYQWFDFAVYSGGVYLEEAYY
YMLGPAKETNIAVFWCLLTVTFSIKMFLTVTRLYFSAEEGGERSVCLTFAFLFLLAMLVQV
VREETLELGLPEGLASMTQNLEPLKKQGDWALPVAKLAIKRVGLAVVGSVLGAFLTFPGLR
LAQTHRDALTMSEDRPMLQFLHTSFLSPLFILWLWTKPIARDFLHQPPFGETRFSLLSDSA
FDSGRLWLLVVLCLLRLAVTRPHLQAYLCLAKARVEQLRREAGRIEAREIQQRVVRVYCYVT
VVSLOYLTPLILTLCNTLLKTLGGYSWGLGPAPLLSPDPSSASAAPIGSGEDEVQQTAAARI
AGALGGLLTPLFLRGVLAYLIWWTAACQLLASLFGLYFHQHLAS

FIGURE 145

CGTTNGCACGCGTCAATGGCGGTCCCTCGGAGTACAGCTGGTGGTGACCTGCTCACTGCCAC
CCTCATGACAGGCTGGCGCCACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAACGGCAGTT
TGTTCCGATACAAGCACCCGNTTGGAGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCC
CAGAGGCAGGAAAAGAGCGGTGGGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCC
GAGATGCCCCGTTCCAGCTGGAGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCTCGCGC
TTCTTCCTGGAGTACCAGTGGTTTGTGGACTTTGCTGTGTACTCGGGCGGCGTGTAACCTCTT
CACAGAGGCCTACTACTACATGCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGT
GCCTGCTCACAGTGACCTTCTCCATCAAGATGTTCTGACAGTGACACGGCTGTACTTCAGC
GCCGAGGAGGGGGGTGAGCGCTCTGTCTGCCTCACCTTTGCCTTCCTCTCCTGCTGCTGGC
CATGCTGGTGCAAGCG

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FIGURE 146

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGCCCCGTGATTATTAACTGGGCTT
 AATCTGAAGGTTCTCAGTCAAATCTTTGTGATCTACTGATTGGGGGGCATGGCAAGGTTTGCTTAAAGGAGC
 TTGGCTGGTTTGGGCCCTTTAGCTGACAGAAGGTGGCCAGGGAGAATGCAGCACATGCTCGGAGAATGAAGG
 CGCTCTCTGTTGCTGGTCTTGCTTGGCTCAGTCTGCTTAACATATGACAAATGTGGGCAACCTGCACCTCTCTG
 TATTAGAATCTGTAAAGGTGCTCCCACTACGGCTGACCAAAGATAGGAAGAGGCGCTCACAGATGGCTG
 TCCAGACGGCTGTGGCAGCTCACAGCCAGGCTCCCTCCCCAGAGGTTTCTGCAGCTGCCACCATCTCCTTAA
 TGACAGACGAGCCTGGCTAGACAACCTGCCTACGTGCTCTCGGCAGAGGACGGGCAGCCAGCAATCAGCCCA
 GTGGACTCTGGCCGGAGCAACCGAATAGGGCACGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTAA
 AAAAAATAATCGAGCTTTGAGTGTCTTCGAAGGACAAAGAGCGGGAGTGCAGTTGCCAACCATGCCAGCCAGG
 GCAGGGAAAATCTGAAAACACCCTGCCCTGAAGTCTTTCCAAGGTTGTACCACTGATTCCAGATGCTGAA
 ATTACCAGCATCAAGATCAATCGATAGATCCCACTGAAAGCCTCTCTATTAGGCTGGTGGGAGGTAGCGAAAC
 CCCACTGGTCCATATCATTTATCCAACACATTTATCGTGATGGGTGATCGCCAGAGACGGCCGGCTACTGCCAG
 GAGACATCATTTAAAGGTCAACGGGATGGACATCAGCAATGTCCCTCACAACCTACGCTGTGGGTCTCTCGCG
 CAGCCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAACAGAAGTTCGCGAGCAGGAACAATGGACAGGCCCC
 GGATGCTCAGACCCCGAGATGACAGCTTTTATGTGATTTCTCAACAAAAGTAGCCCCGAGGAGCAGCTTGGAA
 TAAAACTGGTGGCAAGGTGGATGAGCTGGGCTTTTCAATCTTCAATGTGCTGGATGGCGGTGTGGCATATCGA
 CATGGTCAGCTTGAGGAGAATGACCGTGTGTTAGCCATCAATGGACATGATCTTCGATATGGCAGCCCAAGAA
 TGCGGCTCATCTGATTAGGCCAGTGAAAGACGTGTTACCTCGTCGTGTCGCCAGGTTGGCGAGCGGAGCC
 CTGACATCTTCAGGAAGCCGGCTGGAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGGAGAGGAGCAACAT
 CCCAAGCCCTCCATCCTACAATTACTTGTATGAGAAGGTGGTAAATATCCAAAAGACCCCGGTGAATCTCT
 CGGCATGACCTCGCAGGGGAGCATCACATAGAGAATGGGATTGCTATCTATGTCTCAGTGTGAGCCCG
 GAGGAGTCATAAGCAGAGATGGAAGAATAAAACAGGTGACATTTGTTGAATGTGGATGGGGTGCACATGACA
 GAGGTACGCCGAGTGAGGCAATGATTTGAAAGAACATCATCCTCGATAGTACTCAAAGCTTTGGAAGT
 CAAAGAGTATGAGCCCGAGGAGACTGCAGCAGCCAGCAGCCGTGGACTCCAAACCAACATGGCCCCACCCA
 GTGACTGGTCCCATCTCGGTGATGTGGCTGGAATTACCCGCTGCTGTATTAATGTAAAGATATTGTATTA
 CGAAGAAACACAGCTGGAAGTCTGGGCTCTGCATTTAGGAGGTTATGAAGAATACAATGGAACAAACCTTT
 TTTCTCAATCAATCCTGTTGAAGGAACACCAGCATCAATGATGGAAGAATTAGATGTGGTGATATTTCTCTTG
 CTGTCAATGCTAGAAGTACATCAGGAATGATACATGCTTGTGGCAAGACTGCTGAAAGAATTAAGGAAGA
 ATTACTCTAATATTGTTTCTGGCTGGCCTTTTTTATAGAAATCAATGATGGGTGAGAGGAACACAGAAAAA
 TCACAAATAGCTAAGAAGTGAACACTATATTTATCTTGTCACTCTACACATGTTTATATTTAAAGAAAGATACATTT
 AAAAATGTCAAGAAAGTATGATCATCTAATGAAGGCCAGTTACACCTCAGAAATATGATTCCAAATAATTA
 AAATCTAGTTTTTTCTCAGTGTGGAGATTCTCATTACTCTACACATGTTTATATTTTCTTCTTCAAT
 AAAAGCCCTAAAACACTAAATGATTGTTGTATACCCCACTGAATCAGCTGATTAAATTTAAATTT
 GGTATATGCTGAAGTCTGCCAGGGTACATATGGCCATTTTAAATTACAGTAAATATTTTTTAAATGCA
 TTGCTGAGAAACGTTGCTTTTATCAACAAAGATAAATATTTTTCAGAGTTAA

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FIGURE 147

FIGURE 148

CCAAAGTGATCATTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCT
GCACAGGGCAGCTTTACTTTACTCCAGCACCTTCCTCTCCCAGGCAAATGCTGCTGACCATCT
TTGGGATACAATCTCATGGATACGAGGTTTTTAACATCATCAGCCCAAGCAACAATGGTGGC
AATGTTTCAGGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGC
AGGATCATGCTCTTCTACCACAATTTTTGACTATAAACATGGCTACATTGCATCCAGGGTGC
TCTCCCGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAAT
CTCCAATGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTG
GGTCAAGTACAACCCCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCCTGCTTGGGTCAC
CCATTGAGAACTCTGCAACATATCCCTTTGTATAAGGGGGAAGTGGTTGAAAACACACAT
AATGTCGGTGCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTTGGGAATTTCAATCG
TGCAGACATTCATGTTTAGGATGATTAGCCCTCTGTGTTTATCTTTCAAAGAAATACATCC
TTGGTTTACTCAAAAGTCAAATTAAATCTTTCCCAATGCCCAACTAATTTTGAGATTC
AGTCAGAAAATATAAATGCTGTATTATA

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FIGURE 149

MKILVAFVLVLTIFGIQSHGYEVFNIISPSNNGGNVQETVTIDNEKNTAIVNIHAGSCSSTT
IFDYKHGYIASRVLSRRACFILKMDHQNIPLNQLQWYIYEKQALDNMFSNKYTWVKYNPLE
SLIKDVDWFLLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIHV

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FIGURE 150

GGCACGAGCCAGGAAGTCTCACTGCCCCGAGCAGAGGCCCTACACCCACCGAGGC
ATGGGGCTCCCTGGGCTGTTCTGCTTGGCCGTGCTGGCTGCCAGCAGCTTCTCCAAGGCACG
GGAGGAAGAAATTACCCCTGTGGTCTCCATTGCCTACAAAGTCTTGAAGTTTTCCCAAAG
GCCGCTGGGTGCTCATAACCTGCTGTGCACCCAGCCACCACCGCCCATCACCTATTCCCTC
TGTGGAACCAAGAACATCAAGGTGGCCAAGAAGGTGGTGAAGACCCACGAGCCGGCCTCCTT
CAACCTCAACGTCAACTCAAGTCCAGTCCAGACCTGCTCACCTACTTCTGCCGGGCGTCCT
CCACCTCAGGTGCCCATGTGGACAGTGCCAGGCTACAGATGCACTGGGAGCTGTGGTCCAAG
CCAGTGTCTGAGCTGCGGGCCAATTCACTCTGCAGGACAGAGGGGCAGGCCCCAGGGTGGA
GATGATCTGCCAGGCGTCTCGGGCAGCCACCTATCACCAACAGCCTGATCGGGAAGGATG
GGCAGGTCCACCTGCAGCAGAGACCATGCCACAGGCAGCCTGCCAACTTCTCCTTCTCGCCG
AGCCAGACATCGGACTGTTTCTGGTGCCAGGCTGCAACAACGCCAATGTCCAGCACAGCGC
CCTCACAGTGGTGCCCCAGGTGGTGACCAGAAGATGGAGGACTGGCAGGGTCCCCTGGAGA
GCCCCATCCTTGCCCTGCCGCTCTACAGGAGCACCCGCCGTCTGAGTGAAGAGGAGTTGGG
GGTTTCAGGATAGGGAATGGGGAGGTCAGAGGACGCAAGCAGCAGCCATG**TAGA**ATGAACC
GTCCAGAGAGCCAAGCACGGCAGAGGACTGCAGGCCATCAGCGTGCACTGTTCTGATTGGGA
GTTTCATGCAAAATGAGTGTGTTTTAGCTGCTCTTGCCACAAAAAAAAAAAAAAAAAAAAA

FIGURE 151

MGLPGLFCLAVLAASSFSKAREEEITPVVSIAYKVLEVFPKGRWVLITCCAPQPPPPITYSL
CGTKNIKVAKKVVKTHEPASFNLNVTLKSSPDLLTYFCRASSTSGAHVDSARLQMHWELWSK
PVSELNANFTLQDRGAGPRVEMICQASSGSPITNSLIGKDQVHLQQRPCRQNPANFSFLP
SQTSDWFWCQAANNANVQHSALTVVPPGGDQKMEDWQGPLESPILALPLYRSTRRLSEEEFG
GFRIGNGEVRGRKAAAM

Signal Peptide:

amino acids 1-18

N-glycosylation Sites:

amino acids 86-89, 132-135, 181-184

FIGURE 152

GGTCCTTAATGGCGAGCAGCCGCCGTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTG
 CTGTCCGGCTGGTCCCGGCTGGGCGAGCCGACCCCTCACTCTCTTTGCTATGACATCACCGT
 CATCCCTAAGTTTCAAGCTTGACACGGTGGTGTGCGGTTCAGGCCAGGTGGATGAAAAGA
 CTTTTTCTCACTATGACTGTGGCAACAAGACAGTCACACCTGTGAGTCCCTGGGGAAGAAA
 CTAAATGTCAACCGCTGGAAAGCACAGAACCAGTACTGAGAGAGGTGGTGGACATACT
 TACAGAGCAACTGCGTGACATTGAGCTGGAGAATTACACACCCAAAGGAACCCCTCACCTGC
 AGGCAAGGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGT
 TTCGATGGGCAGATCTTCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCC
 TGGAGCCAGAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCTTCCATT
 ACTTCTCAATGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACC
 CTGGAGCCAAGTGCAGGAGCACCACCTCGCCATGTCTTCAGGCACAACCCAACCTCAGGGCCAC
 AGCCACCACCTCATCCTTTGCTGCCTCCTCATCATCTCCCTGCTTCATCCTCCCTGGCA
 TCTGAGGAGAGTCTTTAGAGTGACAGGTTAAAGCTGATACCAAAAGGCTCCTGTGAGCAG
 GTCTTGATCAAATCGCCCTTCTGTCTGGCCAGCTGCCACGACCTACGGTGATGTCCAGT
 GGCCCTCCAGCAGATCATGATGACATCATGGACCAATAGCTCATTCAGTGCCTTGATTCCTT
 TTGCCAACAATTTTACCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACC
 TGATGGAATTCCTGCACTTAAAGTTCTGGCTGACTAACAAGATATATCATTTTTCTTCTTC
 TCTTTTGTGTTGGAAAAATCAAGTACTTCTTTGAATGATGATCTCTTCTTGCAATGATATT
 GTCAGTAAAATAATCACGTTAGACTTCAGACCTCTGGGGATTCTTCCGTGTCCTGAAAGAG
 AATTTTTAAATTATTTAATAAGAAAAATTTATATTAATGATTGTTTCTTTAGTAATTTAT
 TGTTCGTACTGATATTTAAATAAGAGTTCTATTTCCCAAAAAAAAAAAAAAAAAA

FIGURE 153

MAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCAVQGQVDEKTFLL
HYDCGNKTVTPVSPGLGKKLNVTTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQAR
MSCEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFS
MGDCIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

Important features:**Signal peptide:**

amino acids 1-25

Transmembrane domain:

amino acids 224-246

N-glycosylation site.

amino acids 68-72, 82-86

N-myristoylation site.

amino acids 200-206, 210-216

Amidation site.

amino acids 77-81

FIGURE 154

GGGAAAGCCATTTGAAAACCCATCTATACAACTATATATTTTCATTTCTGCTGCTAGCTG
CCTTGGGCCCTACAATTTTCATTCTGTTTCTGACTTTCAGTTATATACCGTGGAAATGGAG
TTGATCCCAACCATAACATCGTGGAGGGTTTTAATTTGGTGGTAGCCCTCACCCAATTCTG
GTGTGGCTTTCTTTGCAGAGGATTCCACCTTCAAAATCATGAACCTCTGGCTGTTGATCAAAA
GAGAATTTGGATTCTACTCTAAAAGTCAATATAGGACTTGGCAAAAGAAGCTAGCAGAAGAC
TCAACCTGGCCTCCCATAAACAGGACAGATTATTAGGTGATGGCAAAATGGATTCTACAT
CAACGGAGGCTATGAAAGCCATGAACAGATTCCAAAAAGAAAACCTCAAATTTGGGAGGCCAAC
CCACAGAACAGCATTTCTGGGCCAGGCTGTAATCAGAATTGTCGTCGTACATGCTCAACAGC
ATTGCTTTTTTCCCCAAATTAACACATTGTGGAGAAGTGATGATACTCTCCCTTTACCTTT
CCTCTCTCCATTCAAGCATTCAAAGTATATTTTCAATGAATTAACCTTGCAGCAAGGGACC
TTAGATAGGCTTATTCTGACTGTATGCTTTACCAATGAGAGAAAAAATGCATTTCTCTGTAT
CATCCTTTTCAATAAACTGTATTTCATTTGAAAAAAAAAAAAAAAAAAAAA

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FIGURE 155

MELIPTITSWRVLILVVALTQFWCGFLCRGFHLQNHLEWLLIKREFGFGYSKSQYRTWQKKLA
EDSTWPPINRTDYSGDGKNGFYINGGYESHEQIPKRKLKLGQPTEQHFWARL

TEHTT".HTH0660

GTTCTCCTTTCCGAGCCAAAATCCCAGGCGATGGTGAAATTATGAACGTGCCACACC**ATGAAG**
 CTCTTGTGGCAGGTAACTGTGCACACCACCACTGGAAATGCCATCTGCTGCCCTGTCTCTTA
 CCTACCGCGCGAGGTGTGGATTCTGTGTGCAGCCATCGCTGTGCCGCTTACGGCGGGCCC
 AGAAGCTGCCCTCCGTTTGTCTGTGCAGTAACCAAGTTTACGAAGGTGGTGTGCACGCCCGG
 GGCTCTTCCGAGGTCCCGCAGGGTATTCCTCGAACACCCCGTACCTCAACCTCATGGAGA
 CAACATCCAGATGATCCAGGCGACACTTCCGCGACCTCCACCCTGAGGTTCTGTCAGT
 TGGGCAGGAACCTCCATCCGGCAGATTGAGGTGGGGGCTCTTCAACGGCTTGCCACGCTCAAT
 ACCCTGGAGCTGTTGCACAACCTGGCTGCAGCTACCTTACCGGGGCTTTGAATACCTGTCTC
 CAAGTCTCGGGAGCTCTGGCTTTCGAACAACCCCATCGAAGACATCCCCCTTACGCCCTTCA
 ACCGGGTGCCCTCCCTCATGCGCTGGACTTGGGGGAGCTCAAGAAGCTGGAGTATATCTCT
 GAGGGAGCTTTTGAGGGCTGTTCAACCTCAAGTATCTGAACTTGGGCACTGTGCACAACTTAA
 AGACATGCCAACTCTACCCCTCGTGGGGCTGGAGAGCTGGAGATGTGAGGGAACCACT
 TCCCTGAGATCAGGCTTGGTCTCTTCACTGGCTGAGCTCCCTCAAGAAGCTTGGGTATG
 AACTCACAGGTGAGCTTGAATGAGCGGAATGCTTTTACGGGCTGGCTTCACTTGTGGAAT
 CAACTTGGGCCCAATAAACCCTCTCTTCTTTGCCCATGACCTCTTTACCCCGCTGAGGTACC
 TGGTGGAGTGTGCATCTACACCAACCCCTTGAACCTGTGATGTGTGACATCTGTGGGTAGCC
 TGGTGGCTTCGAGAGTATATACCCAACTTCAACCTGCTGTGGCCGCTGTGATGCTCCCAT
 GCACATCGGAGGCCCTACCTCGTGGAGGTGGACACGGCTCTTCCAGTGCTCTGCGCCCT
 TCATCATGAGCGACCACTCGAGACCTCAACATTTCTGAGGTCCGATGGCAGCTTAAAGTT
 CGGACTCCCCCTATGTCTCCGTGAAGTGGTGTGTCGCAATGGGACAGCTGCTCAGCCACGC
 CTCGCCACCCCAAGGATTTCTGTCTCTCAACGACGGCACTTTGAACTTTCCCGAGTGTCT
 TTTACAGACTGGGTGTACATATGATGTGACCACTTTGACGGAACCTTCAACGCTCTCG
 GCTTACTCAATGTGAGACCGGTGAGCTTAAACCTCCAACCTACAGCTTCTTACCACAGT
 AACAGTGGAGACCAAGGAGATCTCGCTGAGGACACACCGGAAGTACAAGCTTGCTTCTTA
 CCAGTCTCACTGGTTACAGCCGGCATATACCACTCTACACGGTGTCTATTCAGACTACC
 CGTGTGCCAAGCAGGTGGCAGTACCCGCGACAGACCACTTGCAGAGATGCAGACCAAGCT
 GGATGAAGTCAATGAAGACCCAGATCATCATTTGGCTGCTTTGTGGCAGTGACTCTGTGAT
 CTGCCGCGATGTTGATGTTCTTCTATAAACTTCTGAAGCGGCACAGCAGCGGAGTACAGTC
 ACAGCCGCGCGGACTGTTGAGATAATCCAGTGGACGAGACATCCAGCAGCAACATCCGC
 AGCAGCAACAGCAGCTCCGTCCGGTGTATGAGTGAGGGGGCAGTAGTGTCTGCCCAATTCT
 ATGACCATTAATCTACACAACTACAAACCTACAAACAGCACATGGGGCCCACTGGACAGAAACAGC
 CTGGGGAACCTCTGTCACCCACAGCTACCACTATCTTGAACCTTATATAATTACAGCCCA
 TACCAAGGACAAGTACAGGAACCTCAAA**TGCA**CTCCCTCCCCAAAAAACTTATAAAT
 GCAATAGAATGCACACAAGACAGCAACTTTTGTACAGAGTGGGGAGAGACTTTTCTTGTA
 TATGCTTATATATTAAGCTCATGGGCTGGTTAAAAAAACAGATTATATAAATTAAAGA
 CAAAAGTCAAAAAC

FIGURE 157

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAAIAAAASAGPQNCPSVCSCSNQFSKVVCT
RRGLSEVPQGI PSNTRYLNL MENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLAS
LNTLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEY
ISEGAFEGFLFNLYLNLGMCNIKDMPNLTPLVGLEELEMMSGNHFPFPIRPGSFHGLSSLKKLW
VMNSQVSLIERNAFDGLASLVELNLAHNNLSSLPHDLFTPLRYLVELHLHHNPWNCDCDILW
LAWWLREYIPTNSTCCGRCHAPMHMRGRYLVEVDQASFQCSAPFIMDAPRDLNISEGRMAEL
KCRTPPMSSVKWLLPNGTVLSHASRHRPRISVLNDGTLNFSHVLLSDTGVYTCMVTNVAGNSN
ASAYLNVSTAELNTSNYSFFTTVTVETTEISPEDTTRKYKPVPTTSTGYQPAYTTSTTVLIQ
TTRVPKQVAVPATDTTDKMQTSLDEVMTTKIIIGCFVAVTLAAAMLIVFYKLRKRHHQORS
TVTAARTVEIIQVDEDI PAATSAATAAPSGVSGEGAVVLP TIHDHINYNTYKPAHGAHWTE
NSLGNLSLHPTVTTISEPYIIQTHTKDKVQETQI

[illegible]

FIGURE 159

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENWNIMCRECCEYDQIECVCPGKREVV
GYTIPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDDFYVKGFYCAECRAGWYGGD
CMRCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRD
GDNRDGQIIKRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFGHAIYEEITACSSSPCFHDG
TCVLDKAGSYKCACLAGYTGORCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTV
VSFFCNSYVLSGNEKRTCQONGEWSGKQPICIKACREPKISDLVRRRVLPMQVQSRETPLH
QLYSAAFSKQKLQSAPTKKPALPFGDLPMPGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGK
WSGRAPSCIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNE
RTVVVAHCVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQSLQISAILHPNYDPILLD
ADIALKLLDKARISTRVQPICLAASRDLSTS FQESHITVAGWNVLADVRSPGFKNDTLRSG
VVSVDLSLLCEEQHEDHGIPVSVTDNMFCAWEPTAPSDICTAETGGIAAVSFPGRASPEPR
WHLMGLVSWSYDKTCSHRLSTAFTKVLFPKDWIERNMK

FIGURE 160

ACCAGGCATTGTATCTTCAGTTGTATCATCAAGTTCGCAATCAGATTGGAAAAAGCTCAACTTGA
 AGCTTTCTTGCCTGCAGTGAAGCAGAGAGATAGATATTATTACAGTAATAAAAAAC**ATGGGC**
 TTCAACCTGACTTTCCACCTTTCCACAAATTCGATTACTGTTGCTGTTGACTTTGTGCCT
 GACAGTGGTGGGTGGGCCACCAGTAAC**TACTTCGTGGGTGCCATTCAAGAGATTCTCTAAAG**
 CAAAGGAGTTCATGGCTAATTTCCATAAGACCCCTCATTTTGGGGAAGGGAAAACTCTGACT
 AATGAAGCATCCACGAAGAAGGTAGA**ACTTGACA**ACTGTCTTCTGTGTCTCCTTACCTCAG
 AGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCACTTTGGAAGAGGTACAGGCAGAAAATC
 CCAAAGTGTCCAGAGGCCGGTATCGCCCTCAGGAATGTAAGCTTTACAGAGGGTCGCCATC
 CTCGTTCCCCACCGGAACAGAGAGAAACCTGATGTACCTGCTGGAACATCTGCATCCCTT
 CCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTATCCACCAGGCTGAAGGTA**AAAAAGT**
 TTAATCGAGCCAACTCTTGAATGTGGGCTATCTAGAGCCCTCAAGGAAGAAAATTTGGGAC
 TGCTTTATATTCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGA
 GGAGCATCCCAAGCATCTGGTGGTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTG
 GATATTTTGGGGGTGTTACTGCCCTAAGCAGAGAGCAGT**TTTTCAAGGTGAATGGATTCTCT**
 AACA**ACTACTGGGGATGGGGAGGCGAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAG**
 AATGAAAATTTCCCGGCCCTGCCTGAAGTGGGTAATATACAATGGTCTTCCACACTAGAG
 ACAAGGCAATGAGGTGAACGCAGAACGGATGAAGCTCTTACACCAAGTGTCA**CAGAGTCTGG**
 AGACAGATGGGTGAGTAGTTGTTCTTATAAAATTAGTATCTGTGGAACACAATCCTTTATA
 TATCAACATCACAGTGGATTCTGGTTGGTGCAT**TCG**ACCTGGATCTTTTGGTGATGTTTGG
 AAGA**CTGATTCTTTGTTTGCAATAATTTTGGCCTAGAGACTTCAAATAGTAGCACACATTA**
 AGAACCTGTTACAGCTCATTGTTGAGCTGAATTTTTCTTTTGTATTTTCTTAGCAGAGCT
 CCTGGTGATGTAGAGTATAAAACAGTTGTAA**CAAGACAGCTTTCTTAGTCATTTTGATCATG**
 AGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAGGAT
 AAAATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTATTTAAATTTGAAGTAATATAT
 TATGGGATAAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCT
 CGTCCAAGGTAGAAAGGTACGAAGATACA**ATACTGTTATTTCATTTATCCTGTACAATCATCT**
 GTGAAGTGGTGGTGTGAGGTGAGAAGCGTCCACAAAAGAGGGGAGAAAAGGCAGCAATCA
 GGACACAGTGA**ACTTTGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTGCGCTGCAAAAGGCAG**
 CAGTAGCTGAGCTGGTGCAGGTGCTGATAGCCTTCAGGGGAGGACCTGCCAGGTATGCCT
 TCCAGTGATGCCACCAGAGAATACATTCTCTATTAGTTTTTAAAGAGTTTTTGTAAATGA
 TTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACATATTAACTAATAATAATA
 TGCTATCAAATACCTCTGTAGTAAATGTGAAAAGCAAAA

FIGURE 161

MGFNLT FHLSYKFRLLLLLTCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLLLGKGMT
LTNEASTKKVELDNCPSPVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRV
AILVPHRNREKHLMYLLEHLHPFLQRQQLDYGIYVIHQAEKKFNRAKLLNVGYLEALKEEN
WDCFIFHDVDLVPENDFNLYKCEEHPKHLVVGRNSTGYRLRYSGYFGGVTTALSREQFFKVNG
FSNNYWGWWGGEDDDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSR
VVRTDGLSSCSYKLVSEHNPLYINITVDFWFGA

Important features:**Signal peptide:**

amino acids 1-27

N-glycosylation sites:

amino acids 4-7, 220-223 and 335-338

Xylose isomerase proteins:

amino acids 191-201

FIGURE 162

CGTGGGCCGGGGTGC GCGAGCGGGCTGTGGGCGCGCCGGAGGAGCGACCGCCGAGTTCTC
 GAGCTCCAGCTGCATTCCCTCCGCGTCCGCCCGACGCTTCTCCGCTCCGGGCCCGCGA**AATG**
 GCCCAGGCGAGTGTGGTCGCGCTCGGCCGCGATCCTCTGGCTTGCTGCCTCTGCCTTGGGCG
 CCCGGCAGGGGTGGCCGAGGCTGTATGAACCTCAATCTCACCCGATAGCCCTGCCACCA
 CGGGAGCGGTGGTGACCATCTCGGCCAGCCTGGTGGCCAAGGACAACGGCAGCCTGGCCCTG
 CCCGCTGACGCCACCTCTACCGCTTCCACTGGATCCACACCCCGCTGGTGCTTACTGGCAA
 GATGGAGAAAGGTCTCAGCTCCACCATCCGTGTGGTCGGCCACGTGCCCGGGGAATTCCCGG
 TCTCTGTCTGGGTCACTGCCGCTGACTGCTGGATGTGCCAGCCTGTGGCCAGGGGCTTTGTG
 GTCTCTCCCATCACAGAGTTCTCTGTGGGGACCTTGTGTCAACCAGAACACTTCCCTACC
 CTGGCCACAGCTCTATCTCACTAAGACCGTCTGAAAGTCTCCTTCTCTCTCCAGACCCGA
 GCAACTTCTCAAGACCGCTTGTCTCTACAGCTGGGACTTCGGGGACGGGACCCAGATG
 GTGACTGAAGACTCCGTGGTCTATTATAACTATTCATCATCGGGACCTTCAACGTGAAGCT
 CAAAGTGGTGGCGAGTGGGAAGAGGTGGAGCCGGATGCCACGAGGGCTGTGAAGCAGAAGA
 CGGGGACTTCTCCGCTCGTGAAGCTGCAGGAAACCTTCAAGCATCCAAGTGTGGGG
 CCCACCTTAATTGACACCTTCCAAAAGATGACGTGACCTTGAAGTCTCTGGGGAGCCCTCC
 TCTGACTGTGTGCTGGCGTCTCAAGCCTGAGTGCCCTCCGCTGGAGGAAGGGGAGTGCCACCC
 CTGTGTCCGTGGCCGACAGCGTACAACCTGACCCACACCTTCAGGACCCCTGGGGAAGTCA
 TGCTTCAGCATCCGGGCGAGAATATCATCAGCAAGACACATCAGTACCACAAGATCCAGGT
 GTGGCCCTCCAGAATCCAGCCGGCTGTCTTTGCTTTCCCATGTGTACTACTTATCACTGTGA
 TGTGTGGCCTTCATCATGTACATGACCTGCGGAATGCCACTCAGCAAAAGGACATGGTGGAG
 AACCCGGAGCCACCTCTGGGGTCAAGTGCTGTGTGCCAGATGTGTGTGGGCCCTTCTTGCT
 GGAGACTCCATCTGAGTACCTGGAATTTGTCGTGAGAACACAGGCGCTGTCTCCGCGCCCTCT
 ATAAGTCTGTCAAACTTACACCGCT**TGA**GCACCTCCCCCTCCCCACCCATCTCAGTGTAA
 CTGACTGCTGACTTGGAGTTTCCAGCAGGGTGGTGTGCACCACTGACCAAGGAGGGTTCATT
 TGCCTGGGGCTGTTGGCCTGGATCATCCATCCATCTGTACAGTTCAAGCACTGCCACAAGCC
 CCTCCCTCTCTGTCAACCCTGACCCAGCCATTACCCATCTGTACAGTCCAGCCACTGACA
 TAAGCCCACTCGGTACACCCCTTGAACCCCTACCTTTGAAGAGGCTTCGTGCAGGACT
 TTGATGCTTTGGGGTGTTCGCTGTGACTCCTAGGTGGGCGCTGGCTGCCACTGCCATTCCT
 CTCATATTGGCACATCTGCTGTCCATTGGGGTCTCAGTTTCTCTCCCCAGACAGCCCTAC
 CTGTGCCAGAGAGCTAGAAGAAGGTCTATAAAGGTTAAAAATCCATACTAAAGGTTGTAC
 ACATAGATGGGCACACTCACAGAGAGAAGTGTGCATGTACACACACCACACACACACACA
 CACACACACACAGAATATAACACATCGCTCACATGGGCATTTAGATGATCAGCTCTGTA
 TCTGGTTAAGTCGTTGCTGGGATGCACCTCGACTAGAGCTGAAAGGAAATTTGACCTCCA
 AGCAGCCCTGACAGGTTCTGGGCCCGGGCCCTCCCTTTGTGCTTTGTCTCTGAGTTCTTCG
 GCCCTTTATAAGGCCATCTAGTCCCTGCTGGCTGGCAGGGGCTGGATGGGGGGCAGGACT
 AATACAGTGAATGTCAGAGTGCTTTATAAATACACTTATTTTATCGAAACCCATCTGTG
 AAACCTTCACTGAGGAAAGGCCCTTGACGCGGTAGAAGAGTTGAGTCAAGGCCGGGCGCGG
 TGGCTCAGCCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCAGCTCAGGACGGA
 GATCGAGACCACCTGGCTGATCAACCGTGAAACCCCGTCTCTACTAAAAAATACAAAAGTT
 AGCCGGGCGTGGTGGTGGTGCTGTAGTCCAGCTACTCGGGAGGCTGAGGCGAGGAGATG
 TGCGAACCCGGGAGGCGGAGCTTGCACTGAGCCAGATGGGCGCACTGCACTCCAGCGTGA
 GTGACAGAGCGAGACTCTGTCTCCA

FIGURE 163

MAQAVWSRLGRILWLACLLPWAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLA
LPADAHLYRFHWIHTPLVLTGKMEKGLSSTIRVVGHPGGEFPVSVWVTAADCWMCQPVARGF
VVLPITEFLVGDLVVTQNTSLPWPSSYLTKTVLKVSEFLHDPNSFLKTALFLYSWDFGDGTQ
MVTEDSVVYNYNSIIIGTFTVKLVVAEWEEVEPDATRAVKQKTGDFSASLKLQETLRGIQVL
GPTLIQTFQKMTVTLNFLGSPPLTVCWRLKPECLPLEEGECHPVSVASTAYNLTHFRDPGD
YCFsIRAENIIISKTHQYHKIQVWPSRIQPAVFAFPcATLITVMLAFIMYMTLRNATQQKDMV
ENPEPPSGVRCCCMCCGPFLLLETPSEYLEIVRENHGLLPPLYKSVKTTYTV

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domain:

amino acids 339-362

N-glycosylation sites.

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

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FIGURE 165

MALSSQIWAACLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTH
FPICIFCCGCCCHRSKCGMCCKT

104111.11100600

FIGURE 166

CTGTCAGGAAGGACCATCTGAAGGCTGCAATTGTGTTCTTAGGGAGGCAGGTGCTGGCCCTGGC
 CTGGATCTTCCACC**ATG**TTCTCTGTGCTGCCTTTTGATAGCCTGATTGTCAACCTTCTGGGC
 ATCTCCCTGACTGCTCTTCCACCTCCTTCTCGTTTTTCATCATAGTGCCAGCCATTTTGG
 AGTCTCCTTTTGGTATCCGCCAACTCTACATGAAAAGTCTGTAAAAATCTTTGCGTGGGCTA
 CCTTGAGAATGGAGCGAGGAGCCAAAGGAGAAGAACCCAGCTTTACAGCCCTACACCAAC
 GGAATCATTGCAAGGATCCCACTTCACTAGAAGAAGAGATCAAAGAGATTCTGCGAAGTGG
 TAGTAGTAAGGCTCTGGACAACACTCCAGAGTTCGAGCTCTCTGACATTTTCTACTTTTGCC
 GGAAAGGAATGGAGACCATATTAGGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAATG
 GAGTCTTGGAACTGCTGAGCAGAACCAATTATAACTTCCAGTACATCAGCCTTCGGCTCAC
 GGTCTGTGGGGGTTAGGAGTGCTGATTCCGGTACTGCTTTCTGCTGCCGCTCAGGATAGCAC
 TGGCTTTTACAGGGATTAGCCTTCTGGTGGTGGGCACAACCTGTGGTGGGATACTTGCCAAAT
 GGGAGGTTTAAGGAATTCATGAGTAAACATGTTCAATGTGTACCAGGATCTGCGTGCG
 AGCGCTGACAGCCATCATCACCTACCATGACAGGGAAAACAGACCAAGAAATGGTGGCATCT
 GTGTGGCCAAATCATACCTCACCGATCGATGTGATCATCTTTGGCCAGCGATGGCTATTATGCC
 ATGGTGGGTCAAAGTGACCGGGGACTCATGGGTGTGATTACAGAGAGCCATGGTGAAGCCGTG
 CCCACACGCTGCTGGTTGAGCGCTCGGAAGTGAAGGATCGCCACCTGGTGGCTAAGAGACTGA
 CTGAACATGTGCAAGATAAAAGCAAAGCTGCCTATCCTCATCTTCCAGAGGAACCTGCATC
 AATAATACATCGGTGATGATGTTCAAAAAGGGAAAGTTTTGAAATTGGAGCCACAGTTTACCC
 TGTGTCTATCAAGTATGACCCCAATTTGGCGATGCCTTCTGGAACAGCAGCAAAATACGGGA
 TGGTGACGTACCTGCTGCGAATGATGACCAGCTGGGCCATTGTCTGCAGCGTGTGGTACCTG
 CCTCCATGACTAGAGAGGCAGATGAAGATGCTGTCCAGTTTGCGAATAGGGTGAAATCTCTG
 CATTTGCCAGGCGAGGAGGACTTGTGGACCTGCTGTGGGATGGGGGCCCTGAAGAGGGAGAAGG
 TGAAGGACACGTTCAAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCGTGGGGAAACCAC
 AAGGACAGGAGCGCTCCT**TGA**GCCTGCCCTCCAGCTGGCTGGGGCCACCGTGCGGGGTGCCAA
 CGGGCTCAGAGCTGGAGTTGCCGCCGCCGCCCACTGCTGTGTCCTTTCCAGACTCCAGGG
 CTCCTCGGGCTGCTCTGGATCCCAGGACTCCGGCTTTTCGCCGAGCCGCAGCGGATCCCTGT
 GCACCCGGCGCAGCCTACCCCTGGTGGTCTAAACGGATGCTGCTGGGTGTGCGACCCAGGA
 CGAGATGCCTTGTTTCTTTTACAATAAGTCGTTGGAGGAATGCCATTAAGTGAACCTCCCA
 CCTTTGCACGCTGTGCGGGCTGAGTGGTGGGGAGATGTGCCCATGGTCTTGTGCTAGAGAT
 GGCAGTACAAGAGTCTGTTATGCAAGCCCGTGTGCCAGGGATGTGCTGGGGCGGCCACCG
 CTCTCCAGGAAGGCACAGCTGAGGCATGTGGCTGGCTTCGGCTCAACATCGCCCCAGC
 CTTGGAGCTCTGCAGACATGATAGGAAGGAACTGTCTATCTGCAGGGGCTTTGAGCAAAATG
 AAGGGTTAGATTTTATGCTGCTGCTGATGGGGTTACTAAAGGAGGGGGAAGAGCCAGTG
 GGCCGCTGACTGGGCCATGGGGAGAACGTGTGTTCTGTAAGCTCAACCTGAACCTCCCC
 ATGTGATGCGCGCTTTGTGTAATGTGTCTCGGTTTCCCATCTGTAATATGAGTCGGGGG
 GAATGGTGGTGAATCTTCTACCTCACAGGCTGTTGTGGGGATTAAAGTGTGTCGGGTGAGTGA
 AGGACACATCACGTTCAAGTACAGGCCCAAAAACGGGGCACGGCAGGCCTGAG
 CTCAGAGCTGCTGCACTGGGCTTTGGATTGTTCTTGTGAGTAAATAAACTGGCTGGTGAA
 TGA

FIGURE 167

MFLLLPFDSLIVNLLGISLTVLFTLLLVFIIVPAIFGVSFGRKLYMKSLLKIFAWATLRME
RGAKEKNHQLYKPYTNGIIAKDPTSLEEEIKEIRRS GSSKALDNTPEFELSDIFYFCRKGME
TIMDDEVTKRFSAAEELESWNLLSRTNYNFQYISLR LTVLWGLGVLIRYCFLLPLRIALFTG
ISLLVVGTTVVGYLPNGRFKEFMSKHVHLMCYRICVRALTAIITYHDRENRPNGGICVANH
TSPIDVIIASDGGYAMVGQVHGGLMGVIQRAMVKACPHVWFERSEVKDRHLVAKRLTEHVQ
DKSKLPILIFPEGTCINNTSVMFKKGSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMVTYL
LRMMTSWAIVCSVWYLP PMTREADEDVQFANRVKSAIARQGGLVDLLWDGGLKREKVKDTF
KEEQQKLYSKMIVGNHKDRSRS

GCCTCTCGAAACCAAGGACTCCAGCACCTCTGGTCCCGCCCTCACCCGGACCCCTGGCCCTCA
CGTCTCCTCCAGG**GATG**CGCGCTGGCGGCTTTGATGATCGCCCTCGGCAGCCTCGCCCTCCAC
ACCTGGCAGGCCCAGGCTGTTCCACCATCTGCCCTGGGCTGGCTCCAGACACCTTTGA
CGATACCTATGTGGTGTGTGCAGAGGAGATGGAGGAGAAGGCAGCCCCCTGCTAAAGGAGG
AAATGGCCACCATGCCCTGCTGCGGGAATCCTGGGAGGCAGCCAGGAGACCTGGGAGGAC
AAGCGTCGAGGGCTTACCTTGGCCCCCTGGCTTCAAAGCCAGAATGGAATAGCCATTATGGT
CTACACCAACTCATCGAACACCTTGTA**CT**GGGAGTTGAATCAGGCCGTGCGGACGGGCGGAG
GCTCCCGGGAGCTCTACATGAGGCACTTTCCCTTCAAGGCCCTGCATTCTACCTGATCCGG
GCCCTGCAGCTGCTGCGAGGCAGTGGGGGCTGCAGCAGGGGACCTGGGGAGGTGGTGTTCCG
AGGTGTGGGCAGCCTTCGCTTTGAACCCAAGAGGCTGGGGGACTCTGTCGCTTGGGCCAGT
TTGCCTCCAGCTCCCTGGATAAGGCAGTGGCCCACAGATTTGGGGAGAAGAGGCCGGGGCTGT
GTGCTGCGCCAGGGGTGCAGCTAGGGTCACAATCTGAGGGGGCTCTCTCTGCCCCCTG
GAAGACTCTGCTCTTGGCCCCTGAGAGATTCCAGCTCTCAGGGGTTGGGCC**TGA**AGTCCA
ACATCTGCCACTTAGGAGCCCTGGGAACGGGTGACCTTCATATGACGAAGAGGCACCTCCAG
CAGCCTTGAGAAGCAAGAACATGGTTCCGGACCCAGCCCTAGCAGCCTTCTCCCCAACAGG
AGTTATGGCCTGGGGAGGCCAGCAGGGCTGAGGGAGCTGCTGCTATGTGATGGGACCTCTCT
GGGACAGCAAGGAAGTACTGAGCAGGCCACTTGATTGAACGGTGTGCAATTGTGGAGACA
TGGAGTTTATTGAGGTAGCTACGTGATTAAATGGTATTGCAGTGTGA

FIGURE 169

MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGCAEEMEKEAAPLLKEEMAHH
ALLRESWEAAQETWEDKRRGLTLPFGKAQNGIAIMVYTNSNTLYWELNQAVRTGGGSREL
YMRHFPFKALHFYLIRALQLLRSGGCSRGPGEVVFRGVGSLRFEPKRLGDSVRLGQFASSS
LDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPWKTLLLAPGEFQLSGVGP

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FIGURE 170

FIGURE 170

FIGURE 171

MAGSPTCLTLIYILWQLTGSAAAGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVT
IQPEGGTIIIVTQNRNRERVDFFDGGYSLKLSKLKNDSGIYYVGIYSSSLQQPSTQEYVLHV
YEHLSPKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISWRW
GESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSLFVLGLFLW
FLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPANTVYSTVEIP
KKMENPHSLLTMPDTPRLFAYENVI

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CTGTGGTCCCAACATGCCTCACCCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCC
TCTGGACCCGTGAAAGAGCTGGTCGGTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTC
CAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTGTGCACCATA
AGCCAGAAGGGGGCACTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCA
GATGGAGGCTACTCCCTGAAGCTCAGCAAACCTGAAGAAGAAATGACTCAGGGATCTACTATGT
GGGGATATACAGCTCATCACTCCAGCAGCCCTCACCAGGAGTACGTGCTGCATGTCTACG
AGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTG
ACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCT
GGGGCAAGCAGCCAATGAGTCCCATATATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAG
AAAGTGATATGACCTTCACTCTGCGTTGCCAGGAACCCCTGTCAGCAGAAACCTTCTCAAGCCCC
ATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCCCTCCATGGTCTGCTT
GTGTCCTCCTGTTGGTGCCCTCCTGCTCAGTCTCTTTGTA CTGGGGCTATTCTTTGGTTTC
TGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGATGGACATTTGTGCGGAA
ACTCTTAACATCTAAGCCCATCTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAA
TAGAACACATCTTAAGGAAGATCCGAGCAAAATACGGTTTACTCCACTGTGGAATACCGAAAA
AGATGAAAAATCCCCCACTCACTGCTCAGCATGCCAGACACACCAAGGCTATTGTGCTATGAG
AATGTTATCTAGACAGCAGTGCCTCCCTAAGTCTCTGCTCAAAAAAAAAAAAAAAAAAAAA

FIGURE 173

GAAAGACGTGGTCCTGACAGACAGACAATCCTATTCCCTACCAAAATGAAGATGCTGCTGCT
GCTGTGTTTGGGACTGACCCTAGTCTGTGTCCATGCAGAAGAAGCTAGTTCTACGGGAAGGA
ACTTTAATGTAGAAAAGATTAATGGGGAATGGCATACTATTATCCTGGCCTCTGACAAAAGA
GAAAAGATAGAAGAACATGGCAACTTTAGACTTTTTCTGGAGCAAATCCATGTCTTGAGAA
TTCCTTAGTICTTAAAGTCCATACTGTAAGAGATGAAGAGTGCTCCGAATTATCTATGGTTG
CTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTTACT
ATACCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTAACGAAAAGGATGGGGA
AACCTTCCAGCTGATGGGGCTCTATGGCCGAGAACCAGATTGAGTTCAGACATCAAGGAAA
GGTTTGCACAACATATGTGAGGAGCATGGAATCCTTAGAGAAAATATCATTGACCTATCCAAT
GCCAATCGCTGCCTCCAGGCCCGAGAATGAAGAATGGCCTGAGCCTCCAGTGTTGAGTGGAC
ACTTCTCACCAGGACTCCACCATCATCCCTTCCTATCCATACAGCATCCCCAGTATAAATTC
TGTGATCTGCATTCCATCCTGTCTCACTGAGAAGTCCAATCCAGTCTATCAACATGTTACC
TAGGATACCTCATCAAGAATCAAAGACTTCTTTAAATTTCTCTTTGATACACCCTTGACAAT
TTTTCATGAAATTATTCTCTTCCTGTTCAATAAATGATTACCCTTGCACTTAA

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FIGURE 174

MKMLLLCLGLTLVCVHAEASSTGRNFNVEKINGEWHTIILASDKREKIEEHGNFRLFLEQ
IHVLENSLVLVKVTVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLI
NEKDGETFQLMGLYGREPDLSSEIKERFAQLCEEHGILRENIIDLSNANRCLQARE

10:11" 11100660

FIGURE 175

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAA
TGGATTGAGCCTGCTGGTTCTACTGCTGTAGGAGTAGTTCTCAATGCGATACCTCTAATTG
TCAGCTTAGTTGAGGAAGACCAATTTTCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTTC
CCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAG
AAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTTCAGTGTGATCA
CAGTCATTGGTGTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAGGTCCTCTC
ATGTGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGA
CATTCATCCAGAATCCTTCAACTTGCAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTG
GTTTCAATAAACCACCAGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCAC
TTCGATTCTGAAGAAAACAACATAGGCTTATCCACTTCTCAGTATTTTtaggtctattgct
TGTTGGAATTCTGGAGGTCCTGTTTGGGCTCAGTCAGATAGTCATCGGTTTCCTTGCGTGTG
TGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTGTGTAGTTTAATGGGAATAAAATGTAAGTA
TCAGTAGTTTGAAAAAAAAA

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FIGURE 176

MTCCEGWTSCNGFSLVLLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMA
IPATMTSLTARKRACCNRTGMFLSSFFSVITVIGALYCM LISIQALLKGPLMCNSPSNSNA
NCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHF DSEENKHRL
IHFSVFLGLLL VGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

134111-1110660

FIGURE 177

GTCGAATCCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACCATGAGGCT
GTCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCCATGCTCTTGTCT
GCCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTC
CAAGTTGCCAAACTTAATCCACCTCCAGAAGCTCTTGACAGCCAAGTTGGAAGTGAAGCACTG
CACCGATCAGATATCTTTTAAGAAACGACTCTCATTGAAAAAGTCTTGGTGGAAATAGTGAA
AAAATGTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTTTCCAAAGTCTTTCAACGACACC
CTGATCTTCACTAAAAATGTAAAGGTTTCAACACGTTGCTTTAATAAATCACTTGCCCTGC

099044-1466

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FIGURE 178

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNLQVAKLNPPPEALAAKLEV
KHCTDQISFKKRLSLKKSWWK

104477-1110660

FIGURE 179

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGG
TGAAGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTG
GAGCAGATCCGTGGGCTGCAGACCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCCCTC
GAACTGTGACATGGGAGAGAGTGACCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGG
AAGCCAATGACCCATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAG
CTGAGCGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGG
CAAATGCAAATACAAGAGCAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCAC
TCATCACTCCAGGCTCTGCCACTACTTGCTTGAGCACAGGACTGGCCTCCAGGGATGGCCTGA
AGCCTAACACTGGCCCCAGCACCTCCTCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTC
TCTCCAAGGGCAGGCTGTTAGGCCCTTTCTGATCAGGAGGCTTCTTTATGAATTAACTCG
CCCCACCACCCCTCA

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FIGURE 180

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCK
YKSSQKQHSPVPEKAIP LITPGSATTC

TDH7T7" hhd660

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGG**ATG**TCGCTGCTGAGCCTGCC
TGGCTGGGCTCAGACCGGTGGCAATGTCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTC
CTGGCTACTCGCCCGCATCTGGCTTGGACCTATGCCTTCTATAACAACCTGCCCGGCTCC
AGTGTTCACACAGCCCCAAACCGGAACCTGGTTTTGGGGTACCTGGGCTGATCACTCCT
ACAGAGGAGGGCTTGAAAGACTCGACCCAGATGTCGCCACCTATFCCAGGGCTTTACGGT
ATGGCTGGGTCCCATCATCCCTTCATCGTTTTATGCCACCTGACACCATCCGGTCTATCA
CCAATGCCCTCAGCTGCCATTGCACCCAAGGATAATCTCTTCATCAGGTTCTCTGAAGCCTGG
CTGGGAGAAGGGATAGTCTGAGTGGCGGTGACAAGTGGAGCCGCCACCTGGGATGCTGAC
GCCCCGCTTCCATTTCAACATCCTGAAGTCTATATAACGATCTTCAACAAGAGTGCAAAACA
TCATGCTTGACAAGTGGCAGCACCTGGCCTCAGAGGGCAGCAGTCTGCTGGACATCTTTGAG
CACATCAGCCTCATGACCTTGGACAGTCTACAGAAATGCATCTTCAGCTTTGACAGCCATTG
TCAGGAGAGGCCAGTGAATATATTGCCACCATTGGAGCTCAGTGCCCTTGTAGAGAAAA
GAAGCCAGGATATCCTCGACGACATGGACCTTTCGTATTACCTCTCCCATGACGGGCGGCGC
TCCACAGGCGCTGCCGCTGGTGCATGACTTCACAGACGCTGTCAATCCGGGAGCGCGCTCG
CACCTCCCCACTCAGGGTATTGATGATTTTTTCAAAGACAAAGCCAAGTCCAAGACTTTGG
ATTTCAATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGGCATTGTCAGATGAGGAT
ATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCAGGCCAGTGGCCTCTC
CTGGGTCTGTACAACCTTCGAGGACCCAGAATACCAGGAGCGCTGCCACAGGAGGTGC
AAGAGCTTCTGAAGGACCGCATCTTAAAGAGATTGAATGGGACGACCTGGCCCAGCTGCC
TTCTTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTTCATCTCCCG
ATGCTGCACCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAGGCATTACCTGCC
TCATCGATATTATAGGGTCCATCACAACCAACTGTGTGGCCGGATCTTGAGGCTCATGAC
CCCTTCCGCTTTGACCCAGAGAACAGCAGAGGGGAGGCTCACCTCTGGCTTTTATCTTTCTC
CGCAGGGCCCAGGAACATGCATGGGCGAGGCTTGCCATGGCGGAGATGAAAGTGGTCTCG
GTTGATGCTGCTGCATTTCCGGTTCTGCGACACCACTGAGCCCCGAGGAAGCTGGAA
TTGATCATGCGCGCCGAGGGCGGGCTTTGGCTGCGGGTGGAGCCCCGTAATGTAGGCTTGCA
GTGACTTTCTGACCATCCACCTGTTTTTTTGCAGATTGTCATGAATAAACCGTGCTGCAAA

MSLLSLPWLGLRPVAMSPWLLLLLVGSGWLLARILAWTYAFYNNCRRLQCFQPQPKRNFWF
HLGLITPTEEGLKDSQMSATYSQGFTVWLGPIIPFIVLCHPDTIRSI TNASAAIAPKDNLF
IRFLKPWLGE GILLSGGDKWSRHRRLTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGS
SRLDMFEHISLMTLSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYY
LSHDGRRFHRACRLVHDFTDAVIRERRRTLPTQGIDDFKDKAKSKTLD FIDVLLSKDEDG
KALSDEDIRA EADTFMFGGHDTTASGLSWVLYNLARHPEYQERCRQEVQELLKDRDPKEIEW
DDLAQLPFLTMCVKESLR LHPPAPFISRCTQDIVLPDGRVIPKGITCLIDIIGVHNPTVW
PDPEYVDPFRFDPENSKGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHT
EPRRKLELIMRAEGGLWLRVEPLNVGLQ

FIGURE 183

CAACAGAAGCCAAGAAGGAAGCCGCTCTATCTTGTGGCGATC**ATG**TATAAGCTGGCCTCCTGC
TGTTTGCTTTTACAGGATTCTTAAATCCTCTCTTATCTCTTCCCTCCTTGACTCCAGGGA
AATATCCTTTCAACTCTCAGCACCTCATGAAGACGCGCGCTTAACTCCGAGGAGCTAGAAA
GAGCTTCCCTTCTACAGATATTGCCAGAGATGCTGGGTGCAGAAAGAGGGATATTCTCAGG
AAAGCAGACTCAAGTACCAACATTTTTAACCCAAGAGGAAATTTGAGAAAGTTTCAGGATTT
CTCTGGACAAGATCCTAACATTTTACTGAGTCATCTTTTGGCCAGAATCTGGAAACCATACA
AGAAACGTGAGACTCCTGATTGCTTCTGGAATACTGTGTC**TGA**AGTGAAATAAGCATCTGT
TAGTCAGCTCAGAAACCCCATCTTAGAATATGAAAAATAACACAATGCTTGATTGAAAAAC
AGTGTGGAGAAAACTAGGCAAACTACACCTGTTTCATTGTTACCTGGAAAAATAATCCTCT
ATGTTTTGCACAAAAA

MYKLASCCLLFTGFLNPLLSPLLDSREISFQLSAPHEDARLTPEELERASLLQILPEMLGA
ERGDILRKADSSTNIFNPRGNLRKFQDFSGQDPNILLSHLLARIWKPKKRETPDCFWKYCV

FIGURE 185

GAACATTTTTAGTTCCCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGAT
GGGGTTGCTGGTTTAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCA
CCACCTCCGCCAGGAACTGCAGGCCACCTGTCTGCAACCCAGCTGAGGCC**ATG**CCCTCCCC
AGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCT
CCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAGCCACCA
GCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCGAAGATGGAGGTCAAGCAGA
AGGGGCAGAGGATGAACTGGAAGTCCGGTTCAACGCCCCCTTTGATGTTGGAATCAAGCTGT
CAGGGGTTCAGTACCAGCAGCACAGCCAGGCCCTGGGGAAGTTTCTTCAGGACATCCTCTGG
GAAGAGGCCAAAGAGGCCCCAGCCGACAAG**TGAT**CGCCCAAGCCTTACTCACCTCTCTCT
AAGTTTAGAAGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGCAACTCCACGACTGTTGTA
CAAGCTCAGGAGGCGAATAAATGTTCAAACCTGTA

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FIGURE 186

MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQVRQQRKESKKPPAKLQPRALAGWLRPEDG
GQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADKO

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FIGURE 187

CGGCCACAGCTGGCATGCTCTGCCTGATCGCCATCCTGCTGTATGCTCCTCGTCCAGTACCTC
 GTGAACCCCGGGGTGCTCCGACGGACCCAGATGTCAAGAATATGAACACGTGGGTGCTGT
 TCCTCCCCCTGTTCCCGGTGCAGGTGCAGACCCTGATAGTCGTGATCATCGGGATGCTCGTG
 CTCCTGCTGGACTTTCTTGGCTTGGTGCACCTGGGCCAGCTGCTCATCTTCCACATCTACCT
 GAGTATGTCCCCACCCTAAGCCCCCGATCCCCCAAGGCTGGGTGGTCAGAGCTGCTCATC
 TTACACCTCTACTTGAGTATGTCCCTAACCTGAGCCCCCAGCCTGGGGCCAGAGTCTTT
 GTCCCCCGTGTGCGCATGTGTTCAGGGTCAGCCTCTCCCAGAAGTGAGATCATGGACAAAA
 GGGCAAAATCACAGGAAGAAATTAATCCATGAGGACCCAGCAGGCCAGCAAGAAGCTGAAC
 TCACGCCGAGACCTGCAGGAGTGGTGCCAGGTGCTTGAAGTAACAAGTTAAATGTTTACA
 GACAATGGAATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTT
 CCAAAACACAAAGTAGAAATTCTAACAATGAAATATATTACAGGCAGGTACCCCACTAACCA
 AACAACCTGAAGCGAGAGCTGTGGTCTTGCTTGGTCTCACAGTGGGCACAGCGGTAGGCGGTC
 AGTCATGTTGCTGAACGACGGAGGGTAAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAGT
 AACAACAACCTCCCTGCTCCTGGCACCAGCCGTTTGGTCATGGTGGGCCAGCTGCAAAGCG
 TCTTCCATTCTCTGGGCAGTGGTGGCCCCGAGGCTGTGGCCTCTCAGGGGTTTCTGTGGAC
 ACGGGCAGCAGAGTGTGTCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTTGGCCA
 ACCCTTGGTCAGGCAGAGGGAGTTGGGTGGGTCAGGCTCTGGGCTCACCTCCATCTCCAGA
 GCATCCCCCTGCCTGCAGTTGTGGCAAGAACGCCAGCTCAGAATGAACACACCCCAACAAGA
 GCCTCCTTGTTTCATAACCACAGGTTACCCTACAAACCACTGTCCCACACAACCTGGGGAT
 GTTTTAAACACACACCTCTAACGCATATCTTACAGTCACTGTTGTCTTGCTGAGGGTTGA
 ATTTTTTTTAAATGAAAGTGCAATGAAATCACTGGATTAAATCCTACGGACACAGAGCTGAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 188

MNTWLLFLPLFPVQVQTLIVVIIIGMLVLLDFLGLVHLGQLLIHFIYLSMSPTLSPRSPQGW
VVRAAHLTPLLEYVPNPPEPTPGARVFPVRMCSGSASPRSEIMDKKGKSQEEIKSMRTQQ
AQQEAEELTPRPAGVPGA




FIGURE 189

GGAGTGCAGATGGCATCCTTCGGTTCTTCCAGACAAGCTGCAAGACGCTGACCATGGCCAAG
 ATGGAGCTCTCGAAGGCCTTCTCTGGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCT
 ATCACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTTGTGGGCACACAGAAGG
 TGCCCAAGCCCCCTGTGCGAGAAAGGTCTGGCAGCCAAGTGCTTTGACATGCCAGTGCCCTG
 GATGGAGATACCAACACATCCACCCAGGAGGTGGTACAATACAACCTGGGAGACTGGGGATGA
 CCGGTTCTCCTTCCGGAGCTTCCGGAGTGGCATGTGGCTATCCTGTGAGGAAACTGTGGAAG
 AACCAGGGGAGAGGTGCCGAAGTTTCATTGAACCTACACCACCAGCCAAGAGAGGTGAGAAA
 GGACTACTGGAATTTGCCACGTTGCAAGGCCCATGTACCCCACTCTCCGATTTGAGGGGAA
 GCGGTTGATGGAGAAGGCTTCCCTCCCTCCCTCCCTTGGGGCTTTGTGGCAAAAATCCTA
 TGGTTATCCCTGGGAACGCAGATCACCTACATCGGACTTCAATTCATCAGCTTCCCTCTGCT
 ACTAACAGACTTGCTACTCACTGGGAACCTGCCTGTGGGCTCAAACCTGAGCGCCTTTGCTG
 CTGTTTCCCTCTGTCTGTCTGCTCAGGTCTCCTGGGGATGGTGGCCACATGATGTATTACAAGTC
 TTCCAAGCGACTGTCAACTTGGGTCCAGAAGACTGGAGACCACATGTTTGGAAATTATGGCTG
 GGCTTCTACATGGCCTGGCTCTCCTTCACCTGCTGCATGGCGTGGCTGTCAACACCTTCA
 ACACGTACACCAGGATGGTGTGGAGTTCAAGTGCAAGCATAGTAAAGAGCTTCAAGGAAAAC
 CCGAACTGCCTACCACATCACCATCAGTGTTTCCCTCGGCGGCTGTCAAGTGCAGCCCCAC
 CGTGGGTCTTTGACCAGCTACCACAGTATCATAATCAGCCATCCACTCTGTCTCTGAGG
 GAGTCGACTTCTACTCCGAGCTGCGGAACAAGGGATTTCAAAGAGGGGCCAGCCAGGAGCTG
 AAAGAAGCAGTTAGGTCATCTGTAGAGGAAGAGCAGTGTAGGAGTTAAGCGGTTTGGGGA
 GTAGGCTTGAGCCCTACCTTACACGTCTGCTGATTATCAACATGTGCTTAAGCCAACATCCG
 TCTCTTGAGCATGGTTTTAGAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTTAAGTC
 CTAAGGGAATTCCTGGGTGCCACTGCTCTCTTTTCCCTCTACAGCTCCATCTGTGTTTACCCAC
 CCCACATCTCACACATCCAGAATCCCTTCTTTACTGATAGTTTCTGTGCCAGGTCTCTGGG
 TAAACCATGGAGATAAAAAGAAGAGTAAATACACTTCCCGACCTTAAGGATCTGAAA

FIGURE 190

MAKMELSKAFSGQRTLLSAILSMLSLSFSTTSLLSNYWFVGTQKVPKPLCEKGLAAKCFDMP
VSLDGDNTSTQEVVQYNWETGDDRFSFRSFRSGMWLSCETVEEPGERCRSFIELTPPAKR
GEKGLLEFATLQGPCHPTLRFGGKRLMEKASLPSPPLGLCGKNPMVIPGNADHLHRTSIHQ
PPATNRLATHWEPCLWAQTERLCCCFLCPVRS PGDGGPHDVFTSLPSCQLGSRRL ETTCLE
LWLGLLHGLALLHLLHGVGCHHLQHVHQDGAGVQVQA

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FIGURE 191

AACTGGAAGGAAAGAAAGAAAGGTACAGCTTTGGCCCA**ATG**TGGTTACCCCTTGGTCTCCTG
 TCTTTATGTCTTTCTCCTCTTCTCTATTCTGTCTATCTCCCTCACTTAAGTCTCAGGCCTGTCA
 GCAGCTCCTGTGGACATTGCCATCCCCTCTGGTAGCCTTCAGAGCAAACAGGACAACCTATG
 TTATGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACCATCTGTGCTTCTGT
 GATCTCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAAATCTGGCATG
 AGATGGCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCCCTGCCCTATTCTCTCCCAA
 GTCTGTTCTCTTATTGTCAACCTCAGCACAACAGGCTGGCGCCAATGGCATTACAGAGAAAG
 CAATCTGTGTGGCTAGTGGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTTGT
 AGCCACCTCCCTGTGAGCCAGTATTAACATGTCCCCTTCCCCTGCCCGCCGTAGATTGAG
 GACATTGCCCTGTGTGCCACCAACCAGGACTTTCCCTTGGCTTGGCATCCCTGGCTCT
 CTCCTGGTACCCAGCAAGACGTCTGTTCAGGGCAGTGTAGCATCTTTCAAGCTCCGTACT
 ATGGCGATGGCCATGATGTTACAATCCCCTTGCCCTGAATAATCAAGTGGGAAGGGGAAGCA
 GAGGGAAATGGGGCCATGTGAATGCAGCTGCTCTGTTCTCCCTACCCTGAGGAAAAACAAA
 GGGGAAGCAACAGGAACCTCTGCAACTGGTTTTATCGGAAAGATCATCTGCCTGCAGATGC
 TGTGAAGGGGCACAAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGGTGTGAAGGAA
 ATAGAACAGTCTGCTGGGAGTCAGACCTGGAATTCTGATTCCAACTCTTTATTACTTTGGG
 AAGTCACTCAGCCTCCCCGTAGCCATCTCCAGGGTGACGGAACCCAGTGATTACTTACCTGCTGG
 AACCAAGGAAACTAACAATGTAGTTACTAGTGAATACCCCAATGGTTTCTCCAATTATGCC
 CATGCCACCAAAACAATAAAACAAAATTCTCTAACACTGAAA

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FIGURE 194

MAGIKALISLSFGGAIGLMFLMLGICALPIYNKYWPLFVLFFYILSPIPYCIARRLVDDTDAM
SNACKELAIFLTGTGIVVSAFGLPIVFARAHLEWGACALVLTGNTVIFATILGFFLVFGSND
DFSWQQW

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[illegible]

FIGURE 196

MDFLLGLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPH
NLSGLLGLSLRYNSLSELRAQQFTGLMQLTWLYLDHNNHICSVQGDAFQKLRRVKELTLSSNQ
ITQLPNTTFRMPNLRSDLSYNKLQALAPDLFHGLRKLTLHMRANAIQFVPVRIFQDCRS
LKFLDIGYNQLKSLARNSFAGLFKLTLEHNDLVKVNFAHFPRLISLHSLCLRRNKVAIV
VSSLDWVWNLEKMDLSGNEIEYMEPHVFETVPHLQSLQLDSNRLTYIEPRILNSWKSITSIT
LAGNLWDCGRNVCALASWLSNFQGRYDGNLQCASPEYAQGEDVLDVYAFHLCEDGAEPTSG
HLLSAVTNRSDLGPPASSATTLADGGEGQHDGTFEPATVALPGGEHAENAVQIHKVVTGTMA
LIFSFLIVVLVLYVSWKCFPASLRQLRQCFVTQRRKQKQKQTMHQMAAMSAQEYYVDYKPNH
IEGALVIINEYGSC TCHQQPARECEV

FIGURE 197

GTGCAAGGAGCCGAGGCGAGATGGGCGTCCTGGGCCGGGTCTGCTGTGGCTGCAGCTCTGC
GCACTGACCCAGGCGGTCTCCAAACTCTGGGTCCCCAACACGGACTTCGACGTCGCAGCCAA
CTGGAGCCAGAACCAGACCCCGTGCGCCGGCGGCCGTTGAGTTCCCGCGGACAGATGG
TGTCAGTCCTGGTGCAAGAAGGTACGCCGTCTCAGACATGCTCCTGCCGCTGGATGGGGAA
CTCGTCCTGGCTTCAGGAGCCGGATTCCGGCGTCTCAGACGTGGGCTCGCACCTGGACTGTGG
CGCGGGCGAACCCTGCCGTCTTCCGCGACTCTGACCGCTTCTCCTGGCATGACCCGCACCTGT
GGCGCTCTGGGGACGAGGCACCTGGCCTCTTCTCGTGGACGCCGAGCGCTGCCCTGCCGC
CACGACGACGTCTTCTTCCGCCTAGTGCTCCTTCCGCGTGGGGCTCGGCCCTGGCGCTAG
CCCCGTGCGTGTCCGCAGCATCTCGGCTCTGGGCCGGACGTTACGCGCGACGAGGACCTGG
CTGTTTTCTGCGCTCCCGCGCGGGCGCCTACGCTTCCACGGGCGGGCGCGCTTGACGCTG
GGCCCCGAGGACTGCGCGGACCCGTGCGGCTGCGTCTGCGGCAACGCGGAGGCGCAGCCGTG
GATCTGCGCGGCCCTGCTCCAGCCCCT

FIGURE 198

MGVLGRVLLWLQLCALTQAVSKLWVPNTDFDVAANWSQNRTPCAGGAVEFPADKMVSVLVQE
GHAVSDMLPLDGELVLASGAGFGVSDVGSHLDCGAGEPAVFRSDRFSWHDPHLWRSIDEA
PGLFFVDAERVPCRHHDDVFFPPSASFRVGLGPGASPVVRVRSISALGRFTTRDEDLAVFLASR
AGRLRFHGPALSVGPEDCADPSGCVCGNAEAQPWICAALLQP

FIGURE 199

[illegible]

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FIGURE 200

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYLSFIP
FARDAVKKCFVCLA

200/330 00000000

FIGURE 201

TTGAGCGCAGGTGAGCTCCTGCGCGTTCCGGGGCGGTTCTCCAGTCAACCTCCCGCGGTTACCCGCGGCGCGC
 CCGAGGGAGTCTCCCTCCAGACCTCCCTCCCGTTGCTCCAACTAATACGGACTGAACGGATCGCTGCGAGGGT
 GGGAGAGAAAATTAGGGGGAGAAAGGACAGAGAGAGCAACTACCATCCATAGCCAGATAGATTATCTTACACTG
 AACTGATCAAGTACTTTGAAAATGACTTCGAAATTTATCTTGGTGTCCCTTCATCTTGCCTGCACTGAGTCTTTC
 AACCACTTTTCTCTCCAATGACACGCAAAAGGTTCTACTACTTTCTTTTGATGGATTCCGTTGGGATTACT
 TATATAAGTTTCCAACGCCCCATTTCATTATATATGAATATGGTGTACGCTGAAGCAAGTTACTAATGTT
 TTTATTACAAAACCTACCCTAACCATTTATACCTTTGGTAAGTGGCCTCTTTGACAGAAATCATGGGATTGTTGC
 AAATGATATGTTTGATCCTATTCCGGAACAAATCTTTCTCCTTGGATCAGTGAATATTTATGATTCCCAAGTTT
 GGGAGAGCGACACCAATATGGATCACAACCCAGAGGGCAGGACATACTAGTGGTGCAGCCATGTGGCCCGGA
 ACAGATGTAAAAATACATAAGCGCTTTCTTACTCATTACATGCCTTACAATGAGTCAGTTTCATTTGAAGATAG
 AGTTGCCAAATTTGTTGAATGGTTTACGTCAAAAGAGCCATAAATCTTGGTCTTCTCTATTGGGAGACCCCTG
 ATGACATGGGCGACCATTTGGGACCTGACAGTCCGCTCATGGGGCTGTCAITTCAGATATTGACAAGAAAGTTA
 GGATATCTCATACAATGCTGAAAAAGGCAAGTTGTGGAACACTCTGAACCTAATCATCACAGTGATCATGG
 AATGACGCGTCTCTGAGGAAGGTTAATAGAACTTGACAGTACCTGGATAAAGACCACTATACCTGATTG
 ATCAATCTCCAGTAGCAGCCATCTTGCCAAAAGAAAGTTAATTTGATGAAGTCTATGAAGCACTAACTCAGCT
 CATCCTAATCTTACTGTTTACAAAAAGAAAGGTTCCAGAAAGGTGGCATTACAAATACAACAGTCCGAATTC
 ACCAATCATAGCAGTGGCTGATGAAGGTGGCACATTTACAGAAATAGTCAGATGACTTTCTGTTAGGCAACC
 ACGGTTACGATAATGCGTTAGCAGATATGCATCCAATATTTTAGCCCATGGTCTCGCTTCAGAAAGAAATTT
 TCAAAAGAGCCATGAATCCACAGATTTGTACCACTACTATGCCACCTCCTCAATATCACTGCCATGCCACA
 CAATGGATCATTCTGGAATGTCAGGATCTGCTCAATTCAGCAATGCCAAGGTGGTCCCTTATACACAGAGTA
 CTATACTCCTCCTGGTATGTTAAACGAGCAGAAATATGACCAAGAGGGGTATACCCCTATTTTATAGGGGT
 TCTCTTGGCAGCATTATAGTGATTGTATTTTTGTAAATTTTCAATTAAGCATTAAATTCAGAGTCAAAATACCTGC
 CTTACAAGATATGCTGCTGAAATAGCTCAACCATTTATACAAGCCCTAATGTTACTTTGAAGTGGATTGTCATA
 TTGAAGTGGAGATTCCATAATTATGTCAGTGTAAAGGTTTCAAATTTGGGAAACCACTTCCAAACATCTGC
 AGAAACCAATTAAGCAGTTACATATTTAGGTATACACACACACACACACACATACACACACACGAGCAAAA
 ATACTTACACCTGCAAGGAATAAAGATGTGAGAGTATGCTCCATTTGTTCACTGTAGCATAGGGATAGATAAG
 ATCTGCTTTAATTTGGAATGCGCAGATAATGTATATTTAGCAACTTTGCATATGTAAAGTACCTTATAT
 ATTGCACTTTAATTTCTCCTGATGGGTACTTTAATTTGAATGCACTTTATGGACAGTTATGCTTATAAC
 TTGATTGAAAATGCAACTTTTGCACCATGTACAGAAATACCTGTTACGATTTGTTCAAACTGAAGGAAAT
 TCTAATAATCCGAAATATGAACATAGAAATCTATCTCCATAAATTGAGAGAAGAAGAGGTGATAAGTGTGA
 AAATTAATGTGATAACCTTTGAACCTGAAATTTGGAGTGTATTCCCAACAGCAGAAATGCAACTGTGGGCAT
 TCTTGTCTAATTTCTTCCAGAGAAGCTGGTTTTCAATTTATTTTCCCTCAAAAGAGAGTCAATATCTGACAT
 ATTGCTCTAATAATATGTTTCTGTCATAAAATATTGTGATTTCCTGATGAGTCATATGCTGATTTTTCA
 TAATAATGAGACACCATGATACTACTTTCTTCTATAGTTCAGCAATGGCCTAATGAGACCAAGCAGGCA
 CCACTCAGCAATGTTTTCTTGTGTTGTAATATTGCTCCTTTGAAAATTAATCACTATTAATTACATTA
 AAATCAAAATGGATAAAAAA

FIGURE 202

MTSKFILVSFILAALSSTTFSLQLDQQKVLVLSFDGFRWDYLYKVPTPHFHYIMKYGVHVK
QVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEEATPIW
ITNQAGHTSGAAMWPGTDVKIHKREPTHYMPYNESVSFEDRVAKIVIEWFTSKEPINLGLLY
WEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHGMTQCSEER
LIELDQYLDKDHYTELIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKEDVPERWHYKYN
SRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTD
LYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSVKPAEYDQEGSYPYF
IGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAETIAQPLLQA

Signal Peptide:

amino acids 1-22

Transmembrane Domain:

amino acids 429-452

N-glycosylation sites:

amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372, 382-385, 389-392

Somatomedin B Domain:

amino acids 69-85

Sulfatase protein Region:

amino acids 212-241

GGATTTTTGTGATCCGCGATTTCGCTCCACGGGCGGGACCTTTGTAAGTCGGGGAGGCCACG
GACAGGCCACCCTGCGGGGCGGGAGGCAGCCGGGTGAGGGAGGTGAAGAAACCAAGACGC
AGAGAGGCCAAGCCCCCTTGCCTTGGGTACACAGCCAAAGGAGGCAGAGCCAGAAGTACAA
CCAGATCCAGAGGCAACAGGGACATGGCCACCTGGGACGAAAAGGCAGTCACCCGCAGGGCC
AAGGTGGCTCCCCTGAGAGGATGAGCAAGTTCTTAAGGCATTCACGGTCGTGGGAGACGA
CTACCATGCTTGAACATCACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGGAGG
AGCAGCCACCACCACACCAAGTCTCAGGCAGGGAAGGCAGAGCTGCAGCCCTGACGTTGCC
CCTGCCCCTGGCCCCGACCCAGGGCCCCCTTGACTTCAGGGGCATGTTGAGGAAACTGTT
CAGCTCCACAGTTCAGGTTCATCATCATCTGCTTGGTGGTTCTGGATGCCCTCCTGGTGC
TTGCTGAGCTCATCTCGGACCTGAAGATCATCCAGCCCGACAGAATAACTATGTCGCCATG
GTATTCACCTACATGAGCATCACCATCTTGGTCTTTTTTATGATGGAGATCATCTTTAAAT
ATTTGTCTTCCGCTGAGTTCTTTCACCACAAGTTTGAGATCCTGGATGCCCGTCGTGGTGG
TGGTCTCATTCCTCGGACATTGTCTCTGTTCCAGGAGCACCAGTTTGAGGCTCTGGGC
CTGCTGATTCTGCTCCGCTGTGGCGGGTGGCCCGGATCATCAATGGGATTATCATCTCAGT
TAAGACACGTTGAGAACGGCAACTCTTAAGGTAAAACAGATGAATGTACAATTGGCCGCCA
AGATTC AACACCTTGAGTTCAGCTGCTCTGAGAAGCCCTGGACTGATGAGTTTGTGTATC
AACCTGTAAGGAGAAGCTCTCTCCGATGGCTATGGGAATGAAGAATCCGACTTCTACTCT
CACACAGCCACCGTGAAGTCTTGAGTAAAATGTGCTGTACAGAAGAGAGAGAAGGAAG
CAGGCTGGCATGTTCACTGGGCTGGTGTACGACAGAGAACCTGACAGTCTGCGCCAGTTA
TCACTTCAGATTACAAATCACACAGGATCTGCTGTTTTCATCAAGAGAACAACAAACC
AAATCTATAAAGATATTCTGAAATATGACAGAATTTGACAAATAAAAGCATAAACGTGTA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 204

MATWDEKAVTRRAKVAPAERMSKFLRHFTVVGDDYHAWNINYYKKWENEEEEEEQPPPTFV
SGEEGRAAAPDVAPAPGPAPRAPLDFRGMLRKLFSHRFQV I I CLVVLDALLVLAELIIDL
K I IQPDKNNYAAMVFHYMSITILVFFMME I I FKL FV FRLSSFTTSLRSWMPVVVVVSFILD I
VLLFQEHQFEALGLLILLRLWRVARIING I I SVKTRSERQLLR LKQMNVLAAKIQHLEFS
CSEKPLD

T0444-11444

CGGCTCGAGCTCGAGCGGAATCGGCTCGAGGGGCAGTGGAGCACCCAGCAGGCCGCCAAC**AT**
GCTCTGTCTGTGCTGTACGTGCGGGTCACTCGGGGAAGGCCAGACGAGTTCCAGTACTTTG
 AGTCGAGAAGGGGCTCCCTCGCGAGCTGAAGTCTCAATTTCAAGCTCAGTGTCTTCACTCCCTCC
 CAGGAATTTCTCCACCTACCCGCGATGGAAAGCGAAAAATTTGATACAGCTCGGAGATGAAGCTC
 TGATGGGCAGCTAGACTTTGAAGAAATTTGTCATTTATCTCCAGATCATCGAAGAAGGCTGA
 GGCTGGTGTTTAGAAATTTTGGACAAAGAAAGATGATGGACGCTATGACGCCCGAGGATGATCG
 CAGTCCCTGCGGGGACTTGGGAGTCAAGATATCTGAACACGAGCGCAAAAAATTTCTTAAGAG
 CATGTGATAAAACCGGCACGATGACCATCGACTGGAAACGAGTGGAGAGACTATCTTAAAGC
 ACCCCGTGAGAAAACCTCCCGAGATACCTCTCTACGGAGACTTTCCAGATTTCTTGATGTC
 GGTGAGAAATCTAACGCTCCCGGATGAGTTCACAGTGGAGGAGGCGAGCAGCGGGATGTGT
 GAGACACCTTGGTGGCAGGAGGTGGGGCGAGGGCGGTATCTCAGAACCTCTACAGGCCCTG
 CAGGCTCAAGGTGCTCATCGAGGTCCATGGCTCCCGCGCAACAACTGGCATGGCATGTGGT
 GGCTTCACTCAGATGATTGAGAAGGAGGGCGCAGGTCACTCTGCGGGGCGAGATCAAGCGC
 CTGCTCAAAATTTGCCCCGAATCAGCCATCAAAATTCATGGCTATGAGGAGCATCAAGCGC
 TTGTTGGTAGTGACACGAGGACTCTGAGGATTCACGAGAGGCTTGTGTCAGGCTCTTGGCA
 GGGGCGCTACGCCACGAGCAGCATCTACCAATGGAGTCTGTGAAGCCCGGATGGCCCTTGCGCA
 GAAGACAGCGCAGTACTCAGGAATGCTGGACTCGCGCAGGAGAGTCTTCCCTATGCGGCATC
 TGGCCGCTTCTCAAAAGGCTATGTCCCAACATCTGCGGCACTGGGCACTTCTCCCTATGCGGCAT
 GACCTTTCGAGTCTACGAGCGCTCAAGAATGCTTGGCTGATGTGCACTACTTCGAGCAGCTGG
 GGACCCGCGGCTGTGTTGTCTCGGGCTGTGGCACTGTGCGGCGCAAGCTCTATTGAGGCGCT
 CCAGTACCCCTTGGCCCTATGTCGAGACCGGATTCAGCGCGTCTGCGGACGAGGGGCCCTTGGGG
 CCGGAGGTGACCATGAGCAGCTCTTCAACAATCTCTCGGACGAGGGGGCCCTTGGGGT
 GTACAGGGGGCTGGCCGCCAACTTCATGATCTATCCACGCTGTGAGCATCAGCTACGCTGG
 TCTACGAGAACCTGAAGATCACCTGGGGCTGCACTCGCGCT**CGA**CGGGGGAGGCGGCCCG
 CGAGTGGACTCGCTGATCTCTGGGCGCAGCTGTGGGCTGTCAGGCACTCTATTCTGTGAATG
 TGGCAACATCAAGCTGTCTGAGCGAGTCTTGAAGAACCTAGACGACCCCGAGGGAGGGT
 GGGGAGGAGCTCGGACGCGCAGGCGCTCTGCTGCTGACCCAGCAGACACCTCTGTGTGGTCT
 AGCGAAGACATCAAGGCTATCTGAGTGGCTGCAATATGAGCTTGGACCTTGGAGGCGCGGCTTGT
 CAGGAGGACATTTTTCAGTGGCTGCGCAATATGAGCTTGGACCTTGGAGGCGCGGCTTGT
 TCTTCCATCTTCACTTCTGGCCAGCTGTGGCCACGGCCCTTGGCTCTGTGCTGGCGGTG
 ATCTCCCTGCTGACCTTCTGCTCTGCTGCTCTGCTGAGTTAAGTGGGAGGAGGCTACAG
 CCCACCTCACGCCCTGCTCAATGCCCAATCATGAAAGTGGAGTTCAGCTGGCTCT
 CAGAGGCTGACTTCCCAACCTACAGCATGAGCCCACTTGGCTGTGAAGGAAGGAAGAAG
 GATTTGGCTTGTGCTACTGTCATGAGCCCTGCTGATGGTGGGGCTCTCGGGATGCT
 TGGGATCGAGGGGGCTGGGCTCTCTCGGCTGGCTGCACAGAAGCAAGTGTGGGGCTCA
 TCTGCTCTGAGCTTGGCTTGACCTTGTCAAGATGGGCGCCACTCAGAACCAAACTCACTG
 TCCCACTGTGGCATGAGGCGAGTGGACAGCTTTGAGGGCGAAGGGCAGAGCGTTTGT
 TGTGCTTGGGAGGGAAGGAAAAAGTTGTGAGGCTTAAATTTGACTGTGGGAAAAAGGG
 TTTTGTCCAGAAGGACAGCGCGACAAATGAGCGACTTCTGTCTCCAGAGGAAGACGAGG
 GAGCAGGAGCTTGGTGACTGCTCGAGAGTCTGTTCTGAGCCTCGGGGGTCTCTGTCCAAC
 CAGCAGGGGCGCAGCGGGAACAGCCCCATCATCTCAATTTGATGTTGATCTGACTCTTCACTTT
 ATTTTGTATTTATTTGAACAGAGTTATGCTCAATATTTTATAGATTTGTTTAAATTAATA
 GCTTGTCAATTTCAAATTTCTTTTATCTATATTTATTTCTATGTTTATGTTTACCTTCCC
 AAGCCGCCAGTGGGATGGGAGGAGGAGGAAGGGGGGCTTGGGCCGCTGCACTCAAT
 CTGTCCAGAGAAATTTCTTTTGGGACTTGGAGGCAAGAGCGGCCACGAAGGCAGCGCCCTG
 GCTCTTTCTCTTGGCAGGTTGGGGAAGGCTTGCCCCAGCCTTAGATTTACGGTTTGA
 CTGGGGGCGTGGAGAGAGAGGAGGAACCTCAATAACCTTGAAGTGGAAATCCAGTTTATTTCT
 CTGCGCTGCAAGGTTTCTTTATTTTCACTCTTCTTGAATGTCAAGGCACTGAGGTGCTCT
 CACTGTGAATTTGCTTGGTGGGCGGGGCTGGAGGAGAGGGTGGGGGGCTGGCTCCCTCCCTCC
 CAGCCTTCTGCTCGGCTTGCTTAACTAGCCGCGCAACTGGCCAGCTCACGGTTGCACTTCC
 ATTTCCACCAAGATGACCTGATGAGGAATCTTCAATAGGATGCAAGATCAATGCAAAATTT
 GTTATATATGAACATAATACTGGAGTCTGTCAAAAGCAAAATGAAGAAGAATTTGGACCTTAG
 AAGTTGTCAATTAAGCAGGCTTCAATAAAGTTGTTTCAAAGCTGAAAAAAGAAAAA
 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA

FIGURE 206

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSIFKLSVFI PSQEFSTYRQWKQKIVQAGDKD
LDGQLDFEEFVHYLQDHEKKLRLVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQA EKILK
SMDKNGTMTIDWNEWROYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTGMW
WRHLVAGGGAGAVSRTCTAPLDR LKVLMOVHASRSNNMGIVGGFTQMIREGGARSLWRGNGI
NVLKIAPESAIKFMAYEQIKRLVGS DQETLRIHERLVAGSLAGAIAQSS IYPMEVLKTRMAL
RKTGQYSGMLDCARRILAREGVAAFYKGYVPNMLGII PYAGIDLAVYETLKNAWLQHYAVNS
ADPGVFVLLACGTMSSTCGQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGA FG
LYRGLAPNFMKVIPAVSISYVVYENLKITLGVQSR

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domain:

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation site.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

[illegible]

[illegible]

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FIGURE 210

MAASLGQVLALVLVAALWGGTQPPLKCRASAGLQRVHEPTWAQQLQEMKTLFLNTEYLMPFLLNQCGLLYLTLASTDLTAVPICNSLAIIFTLIVGKALGEDIGGKRKLDYCECGTQLCGSRHTCVSSFPEPISPEWVRTFPFPLPFPLQLFCFLVAIRVPFPWTVWRKTEAGVWD

TO THE "HINDS"

FIGURE 211

CTTCTGTAGGACAGTCCACCAGGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTG
 GAAGATGACAGCAATTATAGCAGGACCCTGCCAGGCTGTGCGAAAAGATTCCGCAATAAACT
 TTGCCAGTGGGAAGTACCTAGTGAAACGGCCTAAGATGCCACTTCTTCTCATGTCCCAGGCT
 TGAGGCCCTGTGGTCCCATCCTTGGGAGAAGTCAGCTCCAGCACCATGAAGGGCATCCTCG
 TTGCTGGTATCACTGCAGTGCTTGTGTCAGCTGTAGAATCTCTGAGCTGCGTGCAGTGTAAT
 TCATGGGAAAAATCCTGTGTCAACAGCATTGCCTCTGAATGTCCCTCACATGCCAACACCAG
 CTGTATCAGCTCCTCAGCCAGCTCCTCTCTAGAGACACCAGTCAGATTATACCAGAATATGT
 TCTGCTCAGCGGAGAACTGCAGTGAGGAGACACATTACAGCCTTCACTGTCCACGTGTCT
 GCTGAAGAACACTTTTCATTTTGTAAAGCCAGTGCTGCCAAGGAAAGGAATGCAGCAACACCAG
 CGATGCCCTGGACCCTCCCCTGAAAGACGTGTCCAGCAACGCAGAGTGCCCTGCTTGTATG
 AATCTAATGGAAC TTCCTGTGCTGGGAAGCCCTGGAAATGCTATGAAGAAGAAGTGTGTC
 TTTCTAGTTGCAGAACTTAAGAATGACATTGAGTCTAAGAGTCTCGTGTGAAAGGCTGTTC
 CAACGTCAGTAACGCCACCTGTCAGTTCCTGTCTGGTGAAAAACAAGACTCTTGAGGAGTCA
 TCTTTCGAAAGTTTGAGTGTGCAAATGTAAACAGCTTAACCCCCACGCTGCACCAACCACT
 TCCCACAACGTGGGCTCCAAAGCTTCCCTCTACCTCTTGCCCTTGCCAGCCTCCTTCTTCG
 GGGACTGCTGCCCTGAGGTCTGGGGCTGCACCTTGCCAGCACCCCATTTCTGCTTCTCTG
 AGGTCAGAGCACCCCTGCGGTGCTGACACCTCTTTCCTGCTCTGCCCCGTTTAACTGC
 CCAGTAAGTGGGAGTCACAGGTCTCCAGGCAATGCCGACAGCTGCCTTGTTCCTTATTATTA
 AAGCACTGGTTCACTGCCCCAAAAAAAAAAAAAAAAAAAAA

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FIGURE 212

MKGILVAGITAVLVAAVESLSCVQCNSWEKSCVNSIASECPSHANTSCISSASSSLETPVR
LYQNMFCSAENCSEETHITAFTHVHVSAAEHFHFVSQCCQGKECSNTSDALDPPLKNVSSNAE
CPACYESNGTSCRGKFWKCYEEEQCVFLVAELKNDIESKSLVLKGCSNVSNATCQFLSGENK
TLGGVIFRKFEKANVNSLTPTSAPTTSNNGVSKASLYLLALASLLLRGLLP

10411-440660

FIGURE 213

GGCCCTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGAGCGAAGGTAGGAGGCA
 GGGCTTGCCCTCACTGGCCACCCCTCCCAACCCCAAGAGCCAGCCCC**ATg**GTCCCCGCCGCCG
 GCGCGTGCTGTGGGTCTGTGCTGAATCTGGGTCCCCGGCGGCGGGGCCCAAGGCCTG
 ACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTTACGCTTTGGGGGCCCCATGACCCGCAG
 CTACCGGAGCACCGCCCGGACTGGTCTTCCCCGGAAGACAAGGATAATCCTAGAGGACGAGA
 ATGATGCCATGGCCGACGCCGACCGCTGGCTGGACCAGCGGCTGCCGAGCTCTTGGCCGCC
 ACGGTGTCCACCGGCTTTAGCCGGTCGTCCGCCATTAACGAGGAGGATGGGTCTTCAGAAGA
 GGGGGTTGTGATTAATGCCGGAAGGATAGCACCAGCAGAGAGCTTCCAGTGCGACTCCCA
 ATACAGCGGGGAGTTCAGCACGAGGTTTATAGCCAATAGTCAGGAGCCTGAAATCAGGCTG
 ACTTCAAGCCTGCCGCGCTCCCCGGGAGGTCTACTGAGGACCTGCCAGGCTCGCAGGCCAC
 CCTGAGCCAGTGGTCCACACCTGGGTCTACCCCGAGCCGGTGGCCGTCAACCTCACCCACAG
 CCATGCCATCTCCTGAGGATCTGCGGCTGGTGTGATGCCCTGGGGCCCGTGGCACTGCCAC
 TGCAAGTCGGGCACCATGAGCCGGAGCCGGTCTGGGAAGCTGCACGGCCTTTCCGGGCGCCT
 TCAGATTGGGGCGTGAGCCAGCTCCGCACGGAGCACAAAGCCTTGACCTATCAACAATGTC
 CCTGCAACCGACTTCGGGAAGAGTGCCCCCTGGACACAAGTCTCTGTACTGACACCAACTGT
 GCCTCTCAGAGCACCAACAGTACCAGGACCACCACTACCCCTTCCCCACCATCCACCTCAG
 AAGCAGTCCCAGCCTGCCACCCGCCAGCCCCTGCCCAGCCCTGGCTTTTGGAAACGGGTCA
 GGATTGGCCTGGAGGATATTTGGAATAGCCTCTCTTCAAGTTCACAGAGATGCAACCAATA
 GACAGAAACAGAGG**TAA**TGGCCACTTCATCCACATGAGGAGATGTCAGTATCTCAACCTCT
 CTTGCCCTTTCAATCCTAGCACCCACTAGATATTTTTAGTACAGAAAACAAAACCTGGAAAA
 CACAA

FIGURE 214

MVPAAGALLWVLLNLGPRAAGAQGLTQTPTEMQRVSLRFGGPMTRSYRSTARTGLPRKTRI
ILEDENDAMADADRLAGPAAAEALLAATVSTGFSSAINEEDEDGSSEGVVINAGDSTSREL
PSATPNTAGSSSTRFIANSQEPEIRLTSSLPRSPGRSTEDLPGSQATLSQWSTPGSTPSRWP
SPSPTAMPSPEDLRLVMPWGPWHCHCKSGTMSRSRSGKLHGLSGRLRVGALSQLRTEHKPC
TYQQPCPNRLREECPLDTSLCDTNCAQSSTTSTRTTTTFPPTIHLRSSPSLPPASPCPALA
FWKRVRIGLEDIWNSLSSVFTEMQPIDRNQR

TOP SECRET

FIGURE 215

CCCGGGTGACCCACGCGTCCGGGGAGAAAGCATGGCCGGCCTGGCGGCGGTTGGTCCTGCTAGCTGGGGCA
 GCGGCGCTGGCGAGCGGCTCCAGGGCGACCGTGAAGCCGGTGTACCGGAGCTGCGTACTGCAAGTGCAGAGGCA
 GAAGTCTGCTTGGGGGCGCTCTGAATCACTTCCGCTCCGCGCAGCAATCTACATGAGTCTAGCAGGCTGGACCT
 GTGCGGAGCAGCTGTAAAGTATGAGTGTATGTGGGTACCGTGGGCTCTACCTCCAGGAAGTCAAAAGTGCCT
 CAGTTCATGCAAGTGGCCCTTCTCCGCGTCTCTGTTCTTCAAGAGCCGGCATCGGCCGTGGCCTCTGTTCT
 CAATGGCTGGCCAGCTGGTGATGCTCTGCGCGTACCGCACCTTCGTGCCAGCGCTCTCTCCCCATGTACCACA
 CTTGTGTGGCCTTCGCTGGGTGTCCCTCAATGCATGGTCTGTCACACTCTTCCACACCGGAGCACTGAC
 CTCACAGAGAAAATGGACTACTTCTGTGCCTCCACTGTCACTCTACACTCAATCTACCTTGCTGCTGAGGAC
 CGTGGGCGTGCAGCACCCAGCTGTGGTCACTGCTCTCCGCGCTCTCTGCTGCTCATGCTGACCGTGCACGCT
 CCTACCTGAGCCTCATCCGCTTCGACTATGGCTACAACCTGGTGGCCACGTTGGCTATTGGCTGGTCAACGCT
 GTGTGGTGGCTGGCTGGTGCCTGTGGAACAGCGCGGCTGCTCACGTGCGCAAGTGCCTGGTGGTGGTCTT
 GCTGCTGCAGGGGCTGTCCCTGCTCGAGCTGCTTGACTTCCACCGCTCTTCTGGGTCTGGATGCCATGCCA
 TCTGGCACATCAGCACCATCCCTGTCCACGCTCTCTTTTTCAGCTTCTTGGGAAGATGACAGCCTGTACCTGCTG
 AAGGAATCAGAGGACAAAGTCAAGCTGAGCTGAAGAGACCTTGGAGCGAGTCTGCCCGAGTGGGATCCTGCCCC
 GCCCTGCTGGCTCCCTTCTCCCTCAACCTTGAGATGATTTTCTCTTTTCAACTTCTTGAAGTGGACATGA
 AGGATGTGGGCCAGAACTCATGTGGCCAGCCACCCCTGTTGGCCCTCACCAGCCTTGGAGTCTGTTCTAGGG
 AAGGCTCCAGCATCTGGGACTCGAGAGTGGGAGCCCTCTACCTCTGGAGCTGAAGTGGGTGGAAGTGA
 GTGTGTTCTTAGCTCTACCGGGAGGACAGCTGCTGTTCTTCCGCCACAGCCTCTTCCCCATCCCCAGCTG
 CCTGGCTGGTCTGAAGCCCTCTGTCTACCTGGGAGACCAGGACCAAGGCTTAGGGATACAGGGGGTCCC
 CTTCTGTATACCACCCCAACCTCTCCAGGACACCACTAGGTGGTGGTGGATGCTTGTCTTTGGCCAGCCAA
 GGTTCACGGCATCTCCCATGGGATCTTGAGGGACCAAGCTGTGGGATGGGAAGGAGTTTCACTTGACC
 GTTGGCTGAGCAGGTTCCAGGAGGCTCACATACTCCCTTTTCAGGGCCAGGGCTCCAGCAAGCCAGGGCA
 AGGATCTCTGCTGCTGTCTGGTGTAGAGCCTGCCACCGTGTGTGCGGAGTGTGGCCAGGCTGAGTGCATAGG
 TCACAGGCTCTGAGCATGGCATGGTGGTGTGTGAGCTCAGGCTAGGTGCGCAGTGTGGAGAGGGGTGTTGT
 CGGGGAAGAGTGTGGCTTCAAAGTGTGTGTGTGAGGGGGTGGGTGTGTAGCGTGGTGTAGGGGAACGTGTG
 TGCCCTGTGCTGTGGGATGTGAGATGAGTGAAGTCCGGGTGAATGTGTCCACAGTTGAGAGGTTGGAGCAGGAT
 GAGGGAATCTCTACCATCAATATCACTTGTGAGGCGCAGCTCTGCCAAGACGCCACCTGGCGGACAGC
 CAGGAGCTCTCATGGCCAGGCTGCTGTGTGCATGTTCCCTGTGTGTCGCCCTTGGCCCGCTCTGTCAAAAC
 CTCACAGGCTCCCCACACAACAGTGCCTCCAGAAGCAGCCCTTCGAGGCGAGGAGGAGAAATGGGGATGCG
 TGGGGCTCTCTCCATCTCCTTTTCTCTTGGCTTCGATGGCTGGCCTTCCCTTCCAAACCTCCATTCCTCT
 GCTGCCAGCCCTTCTCCATAGCTGATTTTGGGAGGAGGAGGGGCGATTTGAGGGAGAGGGGAGAAAGCT
 ATAGGAATGGAGGAGCTCCAGAACTTTCCATCCCAAGGCAGTCTCCGCTGGTGAAGCAGTGTGATTTTG
 CTCGTGCCCTGACCCCTTGGCCTTTGAGGGAGGGGAGCTATGCTAGGACTCCAACCTCAGGAGCTCGGGTG
 GCTTGGCTAGCTCTTTTGATCTGAAACTTTTAAAGTGGGAGGTTGGCAAGGATGTGCTTAATAATCAAA
 TTCCAAGCCTCAAAAAAAAAAAAAAAAAA

FIGURE 216

MAGLAARLVLLAGAAAALASGSQGDREPVYRDCVLQCEEQNCSGGALNHFRSRQPIYMSLAGW
 TCRDDCKYECMWVTVGLYLQEGHKVPQFHGKWPFSSRFLFFQEPASAVASFLNGLASLVMLCR
 YRTFVPASSPMYHTCVAFAWVSLNAWFWSTVFHTRDTDLTEKMDYFCASTVILHSIYLCCVR
 TVGLQHPAVVSAFRALLLLMLTVHVSYLSLIRFDYGYNLVANVAIGLVNVVWWLAWCLWNQR
 RLPHVRKCVVVVLLQLGLSLELLLDPPPLFWVLDAAHAIWHISTIPVHVLFFSFLEDDSLYLL
 KESDKFKLD

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domains:

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

N-glycosylation site.

amino acids 40-44

N-myristoylation site.

amino acids 43-49

CUB domain proteins profile.

amino acids 285-302

Amiloride-sensitive sodium channels proteins.

amino acids 162-186

[illegible]

FIGURE 218

MAPQSLPSSRMAPLGMLLGLLLMAACFTFCLSHQNLKEFALTNPKESSSTKETERKETKAEEEL
DAEVLEVFPHTHEWQALQPGQAVPAGSHVRLNLQTGEREAKLYEDKFRNNLKGKRLDINTN
TYTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMV
RLINKFNSSSSSLEEKIAALFDLEYVYVHQMDNAQDLLSFGGQLQVVINGLNSTEPLVKEYAAF
VLGAASFSSNPQVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLKL
GGLQVLRITLVQEKGTVEVLAVRVVTLTYDLVTEKMFEEEEAELTQEMSPEKQQYRQVHLLPG
LWEQGWCEITAHLLALPEHDAREKVLQTLGVLLTTCRDYRQDPQLGRTLASLQAEYQVLAS
LELQDGEDEGYFQELLGSVNSLLKELR

Important features:**Signal peptide:**

amino acids 1-29

Hypothetical YJL126w/YLR351c/yhcX family protein.

amino acids 364-373

N-glycosylation site.

amino acids 193-197, 236-240

N-myristoylation site.

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

Homologous region SLS1 protein.

amino acids 68-340

[illegible]

FIGURE 220

MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVIIIVAGAFFWLVSLLLASVVWFILVHVTDR
SDARLQYGLLIFGAAVSVLLQEVFRFAYYKLLKKADEGLASLSEDRSPISIRQMAYVSGLS
FGIISGVFSVINILADALGPGVVGIGDSPYYFLTSAFLTAAIILLHTFWGVVFFDACERRR
YWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQRSLLCKD

104111.4440660

FIGURE 221

AAGCTGGTTTAAAGGAAGCAGAGGAGGGTTAGATTCTGTTGAGTGAGGACGGAAGATCAACCCA
TTTCCATTCCGCCAGATGGCCTATGTTTCTGGTCTCTCCCTTCGGNATCATCAGTGGTGTNT
TNTCTGTTATCAATATTTGGCTGATGCANTTGGGCCAGGTGTGGTTGGGATCCATGGAGAC
TCACCCATTATTCTTGANTTCAGCCTTTNTGACAGCAGCCATTATCCTGCTC

TCTGCTATCCATGGGTGGTGTTCAGTCTCTCCCTTCGGNATCATCAGTGGTGTNT

FIGURE 222

GACCGACCGTTCAGATGCCCGGTTCCAGTACGGCTTCCTGATTTTTGGTGCTGCTGTNTCTG
TCCTTCTACAGGAGGTGTTCCGCTTTGCCTANTACAAGCTGCTTAAGAAGGCAGATGAGGGG
TTAGCATNGCTGAGTGAGGACGGAAGATCACCCATTTCCATCCGCCAGATGGCCTATGTTTN
TGGTNTTTCCTTCGGTATCATCAGTGGTGTTTTNTCTGTTATCAATATTTGGNTGATGCAN
TTGGGCCAGGTGTGGTTGGGATCCATGGAGANTCACCTATTAATTCCTGAATTCAGCCTTT
NTGACAGCAGCCATTATCCTGNTCCATACCTTTTGGGGAGTTGTGTTTTTGTATGCCTGTGA
GAGGAG

00990441-1-14401

FIGURE 223

NGTTGGAGAAGTGGCGGGACNTTCATTGGGGTTTCGGTTTCCCCCTTTCCTTTCCCCG
GGGTCTGGGTGACATTGCACGGGCCCCCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCC
CCAGNTGGNGCGCCCTTCCCATTTCCTGTCTGGTCAGGCCCCACCCCTTCCCACNTG
ACCAGCCATGGGGGCTGCGGTGTTTTTCGGCTGCACTTTCGTGCGTTTCGGCCCGGCTTCG
CGCTTTTCTGTACTGTGGCTGGGGACCGCTTCGCGTTATCATCCTGGTCGCAGGGGCA
TTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTGGTCCATGTGAC
CGACCGGTCAGATGCCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGTCTGTCC
TTCTACAGGAGGTGTTCCGCTTTCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTTA
GCATCGCTGAGTGAGGACGGAAGATCACCATCTCCATCCGCCAGATGGCCTATGTTTCTGG
TCTCTCCTTCGGTATCATCAGTGGTGTCTTCTGTATCAATATTTGGCTGATGCACCTG
GGCCAGGTGTGGTTGGGATCCATGGAGACTCACCC

FIGURE 224

GTAAAAGAAAGTGGCCGGACCTTCATTGGGGTTTCGGTTCCCCCTTTCCCNNTCCCCGGGG
TCTGGGGGTGACATTGCACCGCGCCCNCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCCC
CAGNTGGCGCGCCCTCCCATTTGCCTGTCCTGGTCAGGCCCCACCCCTTCCCACCTGA
CCAGCCATGGGGGCTGCGGTGTTTTTCGGGCTGCACTTTCGTCGCGTTTCGGGCCCGGCCTTC
GCGCTTTTCTTGATCACTGTGGCTGGGGACCGCTTCGCGTTATCATCCTGGTCGAGGGGC
ATTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTGGTCCATGTGA
CCGACCGGTCAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTGGTGTCTGTCTCTGTC
CTTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTT
AGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTG
GTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTGTATCAATATTTTGGCTGATGCACTT
GGGCCAGGTGTGGTTGGGATCCATGGAGAC

FIGURE 225

GCCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCGGTGCCAGAGCCCAGGAGGAGGCAG
 TGGCCAGGAAGGCACAGGCTGAGAAGTCTGCGGCTGAGCTGGGAGCAAAATCCCCACCCCC
 TACCTGGGGACAGGGCAAGTGAGACCTGGTGAGGGTGGCTCAGCAGGCAGGGAAGGAGAGG
 TGTCTGTGCGTCTGCACCCACATCTTTCTCTGTCCCCCTCCTTGCCCTGTCTGGAGGCTGCT
 AGACTCCTATCTTCTGAATTCTATAGTGCCTGGGTCTCAGCGCAGTGCCGATGGTGGCCCGT
 CCTTGTGGTTCCTCTCTACCTGGGGAAATAAGGTGCAGCGGCC**ATG**GCTACAGCAAGACCCC
 CCTGGATGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTTCTGGGGGTACAGAGCATGTT
 CTCGCCAACAAATGATGTTTCTGTGACCAACCCTCTAACACCGTGCCCTCTGGGAGCAACCA
 GGACCTGGGAGCTGGGGCCGGGAAGACGCGCCGGTGGATGACAGCAGCAGCCGCATCATCA
 ATGGATCCGACTGCGATATGCACACCCAGCCGTGGCAGGCCGCGCTGTGCTAAGGCCCAAC
 CAGCTCTACTGCGGGGCGGTGTTGGTGCATCCACAGTGGCTGCTCACGGCCGCCACTGCAG
 GAAGAAAGTTTTAGAGTCCGTCTCGGCCACTACTCCCTGTACCCAGTTTATGAATCTGGGC
 AGCAGATGTTCCAGGGGTCAAATCCATCCCCACCTGGCTACTCCACCTGGCCACTCT
 AACGACCTCATGCTCATCAAACCTGAACAGAAGAATTGCTCCCACTAAAGATGTCAGACCCAT
 CAACGTCTCCTCTCATTTGTCCTCTGCTGGGACAAAGTGCTTGGTGTCTGGCTGGGGGACAA
 CCAAGAGCCCCCAAGTGCACTTCCCTAAGGTCTCCAGTGCTTGAATATCAGCGTGCTAAGT
 CAGAAAAGGTGCGAGGATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGA
 CAAAGCAGGTAGAGACTCCTGCCAGGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCC
 TGCAGGGACTCGTGCTCTGGGGAGATTACCCCTGTGCCCCGCCCAACAGACCGGGTGTCTAC
 ACGAACCTCTGCAAGTTCACCAAGTGGAATCCAGGAAACCATCCAGGCCAACTCC**TGA**GTGTCAT
 CCCAGGACTCAGCACACCGGCATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTTTCAG
 ACCCTCATTCCTTCCCAGAGATGTTGAGAATGTTCTATCTCTCCAGCCCTGACCCCATGTCT
 CCTGGACTCAGGGTCTGCTTCCCCACATTGGGCTGACCGTGTCTCTCTAGTTGAACCCTGG
 GAACAATTTCCAAAACGTCCAGGGCGGGGGTTCGCTCTCAATCTCCCTGGGGCACTTTTCAT
 CCTCAAGCTCAGGGCCCATCCCTTCTCTGCAGCTCTGACCCAAATTTAGTCCAGAAATAAA
 CTGAGAAGTGAAAAAAA

FIGURE 226

MATARPPMMWVLCALITALLGVTEHVLANNNDVSCDHPSNTVPSGSNQDLGAGAGEDARSDD
SSSRIINGSDCDMHTQFPWQAALLLRPNQLYCGAVLVHPQWLLTAAHCRKKVFRVRLGHYSLS
PVYESGQQMFQGVKSIPHPGYSHPGHSNDLMLIKLNNRRIRPTKDVRPINVSSHCP SAGTKCL
VSGWGTTKSPQVHF PKVLQCLNISVLSQKRCE DAYPRQIDDTMFCAGDKAGR DSCQGD SGGP
VVCNGSLQGLVSWGDYPCARPNRPGVYTNLCKFTKWIQETIQANS

FIGURE 227

ATGTCTCAACGACCGGTGGAAGACCATGGGCGGCGCTGCCAACCTTGAAGACCGGCCGCGCGCA
 CAAGCCGAGCGGCCGAGCTGCGGCTACGTGCTGTGCACCGTGTGTGCGCCCTGGCTGTGC
 TGCTGGCTGTAGCTGTACCGGTGCCGTGCTCTTCTGAACACGCGCCACGCGCCGGGACAG
 GCGGCCCACTGTGCTCAGCACTGGGGCTGCCAGCGCCAACAGCGCCCTGGTCACTGTGGA
 AAGGGCGGACAGCTCGCACTCAGCATCTCTATTGACCCGCGCTGCCCGAGCTACCCGACA
 GCTTCGCAAGCCCTGGAGAGCCGCCAGGCTCGGTGCTGCAAGCGCTGACAGAGCACCAGGCC
 CAGCCACGCTGTGTGGCGACGAGGAGCAGGAGCTGCTGGACAGCTGGCCGACCAAGTGC
 CGCGCTGGCGCCAGGCCCTCAGCGCCTGCAGAGTGAGCAGGGCGCCCTCATCCAGCTTCTC
 GCACGCTGGCGCCAGGCCCATGGCTCACCCTGGTGAACCTCCGTACGCGACATCTGGATGCCCT
 TCTGAGAGACCGGGGCTGGGCGGCGCCGCAACAAGGCCGACCTTCAGAGAGCGCTGCC
 GCAGAGGGACCGGGGCTGGGCGGCGCCGCAACAAGGCCGACCTTCAGAGAGCGCTGCC
 GGGGACCCGCGCCCGGGGCTGTGCCACTGGCTCCCGGCCCGGAGACTGTCTGGACGTCTCT
 CTAAGCGGACAGGACGATGGCGTCTACTGTCTTTCCACCCACTACCGGCCGCGCTT
 CCAGTGTACTGTGACATGCCGACGGACGGCGGCGCTGGACGGTGTTCAGCGCCGGGAGG
 ACGGCTCCGTGAACCTTCTCCGGGCTGGGACGCGTACCGAGAGCGCTTGGCAGGCTCAC
 GGGGAGCACTGGCTAGGGCTCAAGAGGATCCACGCCCTGACCACACAGGCTGCCTACGAGCT
 GCACCTGGACCTGGAGGACTTTGAGAATGGCAGGCGCTATGCCGCTACGGGAGCTTCGGCG
 TGGGCTGTCTCCGTGGACCTGAGGAAGACGGGTACCGCTACCGTGGCTGACTATTC
 GGCACCTGCAGGCACTCCCTCTGAAGCACAGCGGATGAGGTTACACACCAAGGACCGTGA
 CAGCGACCATTCAGAGAACAACTGTGCCGCTTCTACCGCGGTGCTTGGTGTACCGCACT
 GCCACAGCTTCAACCTCAATGGGCACTACCTGCGCGGTGCGCAGCGCTTCTATGCCGAGCG
 GTGGAGTGTCTCTTGACCGGCTGGCAGTACTCAAGTTCCTGAGATGAAGATCCG
 GCCGTCGCGGAGGACCG**TAG**ACTGGTGCACCTTGTCTTGGCCCTGCTGGTCCCTGTGCG
 CCCCTCCCGACCCCACTCTACTTTCGTGAATGTCTCCACCCCACTGTGCCTGGCGGAC
 CCACCTCCAGTAGGGAGGGCGCGGCCATCCCTGACACGAAGCTCCCTGCCCTGCCCACTGTGACTCCGG
 CACACATCGCTTCTCGCGCTCCCAACCCCTCCATTTGGCAGCTCACTGATCTCTTGCCTC
 TGCTGATGGGGGCTGGCAAACTTGACGACCCCACTCTGCTTGGCCCACTGTGACTCCGG
 TGCTGTTTGGCGTCCCTGGCCAGGATGGTGGAGTCTGCCCGAGGCACTCTGCCCTGCC
 GCGCAAAATACCGGCATTATGGGGACAGAGAGCAGGGGGCAGACAGCACCCTGGAGTCTCT
 CTAGCAGATCGTGGGGAATGTCAAGTCTCTCTGAGGTCAAGTCTGAGGCCAGTATCTCCAG
 CCTCCCAATGCCAACCCCACTTCCCTGGTGGCCAGAGAACCCCTCTCCCCCAA
 GGGCTCAGCTGGCTTGGGCTGGGTGGCCCATCTACAGGCGCTGAGGTCAAGGATGGG
 GAGCTGCTGCTTTGGGAGCCACGCTCCAAGGTGAGACCACTTCCCTGGAGGCCACCCAC
 CTTGTGCCCGGAGGCGTGGGTCTGCAGTCTCTTACCTGCTGTGCCCACTGTCTCTGT
 TCTCAAATGAGGCCAACCCATCCCCACCACTCCCGGCCCTCTCTACCTGGGGCAGC
 CGGGCTGCCATCCCACTTCTCTGCTTGGAGGTGGGTGGGGCCCTGCACCGTGGGGCT
 GGACTGCGCTAATGGGAAGCTTGTGTTTCTGGGCTGGGGCTAGGAGGGCTGGGATGAG
 GCTTGTCAACACCCCAACCAATTTCCAGGGACTCCAGGGTCTGAGGCCCTCCAGGAGG
 GCTTGGGGGTGATGACCTTCCCTGAGGTGCTGTCTCATGAGGAGGCCAACCTTCC
 ATTGACCGTGGCCACTGGACCCAGGCCAGGCCCGGCCCGCGAGTGGTCAAGGGACAGGGA
 CCACTCACCGGGCAAAATGGGTGCGGGGACTGGGGCACCAGCAGGCACTGGACA
 CTTTGTGTTGAATCTCCCAACACCCAGCACGCTGTCTATCCCACTCTTGTGTGCACACA
 TCGAGAGGTGAGACCCGAGGCTCCAGGACCCAGCAGCCACAAGGCCAGGGCTGGAGCGGG
 TCCCTCAGCTGTCTCTCAGCAGCCTGGACCCGCGTGCCTTACGTGAGGCCAGATGCGAGG
 CGGCTTTTCAAGGCCTCTGATGGGGCTCCGAAAGGGCTGGAGTCAAGCTTGGGAGCT
 GGCTAGCAGCTCTCTCGGGCAGGAGGGGAGGTGGCTTCTCCAAAGGACACCCGATGGCA
 GGTGCTAGGGGTGTTGGGTTCCGTTCTCCCTTCCCTCCCACTGAAGTTTGTGCTTAA
 AACAATAAATTTGACTTGGCACCCTGGGGGTTGGTGGGAGAGGCCGTGTGAGCTGGCTCT
 TGTCACAGTGCCACCAAGTTCACATGCGCAG

FIGURE 228

MVNDRWKTMGAAQLED RPRDKPQRPSCGYVLCTVLLALAVLLAVAVTGAVLFLNHAHAPGT
APPPVVSTGAASANSALVTVERADSSHL SILIDPRCPDLTDSFARLESAQASVLQALTEHQA
QPRLVGDQEQLD LDTLADQLPRLARASELQTECMGLRKHGHTLGQGLSALQSEQGRLIQLL
SESQGHMAHLVNSVSDILDALQDRGLGRPRNKADLQAPARGTRPRGCATGSRPRDCLDVL
LSGQQDDGVYSVFPTHYPAGFQVYCDMRTDGGGWTVFQRREDGSVNFFRGWDAYRDGFGRLT
GEHWLGLKRIHALTTQAAAYELHVDLEDFENGTA YARYGSFGVGLFSVDPEEDGYPLTVADYS
GTAGDSLLKHSGMRFTTKDRSDHSENNCAAFYRGAWWYRNCHTSNLNGQYLRGAHASADG
VEWSSWTGWQYSLKFSEM KIRPVREDR

FIGURE 229

GCAGTCAGAGACTTCCCTGCCCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCCT
 TGCTTCTGAAGTACAGTACAGTAGCCCGCGGCCAGGGCAATCCGACCACATTTCACTCT
 CACCGCTGTAGGAATCCAGATGAGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATG
 ATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCC
 CGGCGCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCCTGCTGAC
 TTTGTGCTTGGTGTCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTACTACC
 AGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATACGTCC
 CAAGAGTTGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGC
 TGAAAAAAGTCTGTCTGAGCTGTATAACAAGCTGGAGCACAGGTGCAGCCCTTGTACAG
 AACAAATGGAATGGCATGGAGACAATTGTACAGTCTTATAAAGACAGCAAAAGTTGGGAG
 GACTGTAATATTTCTGCCTTAGTGAAGTCTTACCATGCTGAAGATAAACAAGAAAGA
 CCTGGAATTTGCGCGCTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTT
 TGCGCCCTGACAGTGGCAAGGCTGGCTGTGGATGGATGGAACCCCTTCACTTCTGAAGT
 TTCCATATTATAATAGATGTCAAGGCCAAGAGCAGAGACTGTGTGGCCATCTCAATGG
 GATGATCTTCTCAAAGGACTGCAAAAGAAATGAAGCGTTGTGTCTGTGAGAGAAGGGCAGGAA
 TGGTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACTGATTCGCC
 CTCTGCAACTACAAATAGCAGAGTGAAGCAGGCGGTGCCAAGCAAGGGCTAGTTGAGACAT
 TGGGAAATGGAACATAATCAGGAAAGACTATCTCTGACTAGTACAAAATGGGTTCTCGTG
 TTTCTGTTCAGGATCACCAGCATTTCTGAGCTTGGGTTTATGACGTTATTAACAGTACAA
 AGAAGTCTTATTTACATGCCACCAACCACTCAGAAACCCATAATGTCTCTGCCTTCTTG
 GCTTAGAGATAACTTTTAGTCTCTTCTCTCAATGTCTAATATCACCTCCCTGTTTTCTAT
 GTCTTCTTACACTTGGTGAATAAGAACTTTTTGAAGTAGAGGAAATACATTGAGGTAAC
 ATCCTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATGGCAGTCACTTCCAGATTTGTACC
 AGCAATACACAAGGAATTTTTTTGTTGTTTCAGTTCATACTAGTCCCTTCCCAATCCAT
 CAGTAAAGACCCCATCTGCCTTGTCCATGCCGTTTCCCAACAGGGATGTCACTTGATATGAG
 AATCTCAAATCTCAATGCCTTATAAGCATTCCTTCTGTGTCCATTAAAGACTCTGATAATTG
 TCTCCCTCCATAGGAATTTCTCCAGGAAAGAAATATATCCCCATCTCCGTTTCATATCAG
 AACTACCGTCCCCGATATTCCCTTTCAGAGAGATTAAAGACCAGAAAAAGTGAGCCCTTCA
 TCTGCACCTGTAATAGTTTCAGTTCCTATTTTCTCCATTGACCCATATTTATACCTTTCAG
 GTACTGAAGATTTAATAATAATAAATGTAATACTGTGAAAAA

FIGURE 230

MQAKYSSTRDMLDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSSTWRPVALTLLTLCVLVLL
IGLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRE
LYNKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAAS
QSYSEFFYSYWTGLLRPDSGKAWLWMDGTPFTSELFHIIIDVTSPRSRDCVAILNGMIFSKD
CKELKRCVCERRAGMVKPESLHVPPETLGEGD

204311.4400660

AATTTTCACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCAGAGGGACATGNTGG
 ATGATGATGGGACACCACCATGAGCCTGCATTNTCAAGCTTTTGCCACAATTGCGCATCCAG
 AGCCCCGGCGCACAGAGCACAGGGNTCCTTTTTTCAACGTGGCGACCAGTGGCCCTGACCTTG
 CTGACTTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTA
 CTACCAGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATA
 CGTCCCAAGAGTTGCAATTTNTTCAAGTCCAGAATATAAAGCTTGCAGGAAGNTGCAGCAT
 GTGGCTGAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGGAACCTTTGAAGGAGGGCAA
 AGTNTCCTCATNTACTATACACACACCACCTTCCC

FIGURE 232

CGCGAGCGCAAGAACCTGCGCAGCCCCAGAGCAGCTGCTGGAGGGGAAATCGAGGGCGCGCTC
 CGGGGATTCGGCTCGGGCGCTGGCTCTGCTCTGCGGGGAGGGAGCGGGGCCCGCGCGGGG
 CCCGAGCCCTCCGGATCCGCCCCCTCCCCGGTCCCGCCCCCTCGGAGACTCTCTTGCTGGCTGCT
 CTGGGGATTCCGCGGGGCGGGGACCGCGGTCGCGGGCGCC**ATG**CGGGCATCGCTGCTGCTG
 TCGGTGCTGCGGGCCGCGAGGGCCCGTGCCCGTGGGCATCTCCCTGGGCTTACCCGTGAGCCT
 GCTCAGCGCTCAGCTGGTGGAGGAGCCGTGCGGCCAGGCCCGCCCAACCTGGAGACTCTG
 AGCTGCCGCCGCGCGGCAACACCAACGCGGCGCGCCGCGCCCAACTCGGTGCAGCCCGGAGCG
 GAGCGCGAGAAGCCCGGGGCGGGCGAAGGCGCGGGGAGAATTGGGAGCCGCGCTTTCGCC
 CTACCACCTTGACAGCCCGGCCAGGCCGCCAAAAAGGCCGTGAGGACCCGCTACATCAGCA
 CGGAGCTGGGCATCAGGCAGAGGCTGCTGCTGGCGGTGCTGACCTCTCAGACCACGCTGGCC
 ACGCTGGGCGTGCCCGTGAACCGCACGCTGGGGCACCGGCTGGAGCGTGTGGTGTTCCTGAC
 GGGCGCAGCGGGCCGCGGGGCCCACTGGCATGGCAGTGGTGACGCTGGGCGAGGAGCGAC
 CCATTGGACACCTGCACCTGGCGCTGCGCCACCTGCTGGAGCAGCACGGCGACGACTTTGAC
 TGGTCTTCCTGGTGCCTGACACCCTACACCGAGGCGCACGGCTGGCAGCCCTAACTGG
 CCACCTCAGCCTGGCTCCGCGGCCACCTGTACCTGGGCGGGCCAGGACTTATCGGCG
 GAGAGCCACCCCGGCCCTACTGCCACGGAGGCTTTGGGTGCTGCTGTGCGCGCATGCTG
 CTGCAACAACCTGCGGCCCACTTGAAGGCTGCCGCAACGACATGCTGAGTGGCGCCCTGA
 CGAGTGGCTGGGTGCTGCTGCTGATGCCACCGGGTGGGCTGCATGGTGACCACGAGG
 GGGTGCACTATAGCCATCTGGAGCTGAGCCCTGGGGAGCCAGTGAGGAGGGGGACCCCTCAT
 TTCCGAAGTGCCCTGACAGCCACCCCTGTGCGTGACCTGTGCAGATGTACAGACTGCAACA
 AGCTTTCCGCCCGAGCTGAAGCTGGAACGCAAGTACCAGGAGATCCAGGAGTACAGTGGGAGA
 TCCAGAATACGAGCCATCTGGCCGTTGATGGGGACCGGGAGCTGCTTGGCCCGTGGGTATT
 CCAGCACCATCCCGCCCGGCTCCCGCTTTGAGGTGCTGCGCTGGGACTACTTACGGGAGCA
 GCACGCTTCTCCTGCGCCGATGGCTCACCCCGCTGCCACTGCGTGGGGCTGACCGGGCTG
 ATGTGGCCGATGTTCTGGGGACAGCTCTAGAGGAGCTGAACCGCCGCTACCACCCGGCCTTG
 CGGCTCCAGAAGCAGCAGCTGGTGAATGGTACCGAGCCTTGATCCGCGCCGGGTATGGA
 ATACAGCTGGACTTGCAGCTGGAGGCATGACCCCCAGGGAGGCGCGCGCCCTCACTC
 GCCGAGTGACGCTGCTCGGCCGCTGAGCCGCTGGAGATCTTGCTGTGCCCTATGCTCACT
 GAGGCCCTCAGCTCTCACTGTGCTGCTGCTTACGTGCGGCTGAGCGTGACCTGCCCCCTGG
 CTTCTTGGAGGCCTTTGCCACTGCAGCACTGGAGCCTGGTGATGCTGGGCGAGCCCTGACCC
 TGCTGCTACTGTATGAGCCGCGCCAGGCCAGCGCGTGGCCCATGCAGATGTCTTGCACTT
 GTCAGGCCCCACGTGGCAGAGCTGGAGCGCGCTTCCCGGCTGCCCGGTGCCATGGCTCAG
 TGTGCAGCAGCCGACCCCTCACCACTGCGCCTCATGGATCTACTCTCAAAGAAGCACCCG
 TGGACACACTGTTCTGCTGGCGGGGCCAGACCGGTGCTCACGCCTGACTTCTTGAACCCG
 TGCGCATGCATGCCATCTCCGCTGGCAGGCCCTTCTTTCCCATGACTTTCCAGACTTCCA
 CCCAGGTGTGGCCCCACCAAGGGCTGGGCCCCAGAGCTGGGCGGTGACACTGGCCGCT
 TTGATCGCAGCAGCAGCGAGGCGCTGCTTCTACAACCTCCGACTACGTGACGCGCCGTGGG
 CGCTTGGCGGAGCCTCAGAAACAAGAGGAGCTGCTGGAGAGCCTGGATGTGTACGAGCT
 GTTCTCTCACTTCTCAGTCTGCATGTGCTGCGGGCGGTGGAGCCGCGCTGCTGCAGCGCT
 ACCGGGCCCACTGTGACGCGGAGGCTCAGTGAGGACCTGTACCAACCGCTGCCCTCAGAGG
 GTGCTTGAGGGCCCTGGCTCCCGAACCCAGCTGGCCATGCTACTCTTTGAACGAGGAGCAGG
 CAACAGCACC**TGA**CCCCACCTGTCCCCGTGGCGATGGCCATGGCCACACCCCAACCCACTT
 CTCCCCCAAACCAGAGCCACCTGCCAGCCTCGCTGGGCGAGGCTGGCCGTAGCCAGACCCC
 AAGCTGGCCCCACTGGTCCCTCTCTGGCTCTGTGGGTCCCTGGGCTCTGGACAAGCACTGGG
 GGAGCTGCCCCAGAGCAACCCACTTCTCATCCCAAACCCAGTTTCCCTGCCCCCTGACGCT
 GCTGATTCCGGCTGTGGCCTCCACGTATTATTGACAGTACAGTCTGCGCTGACGCGCAGCCGTG
 CTCCTGGGCCCCGGGGCTGGGCTGTAGAAGAGTTGTTGGGGAAGGAGGAGCTGAGGAGGGG
 GCATCTCCCAACTCTCTCCCTTTTGGACCCCTGCCGAAGCTCCCTGCCTTTAATAAACTGGCCA
 AGTGGGAAAAA

FIGURE 233

MRASLLLSVLRPAGPVAVGISLGFTLSLLSVTWVEEPCGPGPPQPGDSELPPRGNTNAARRP
NSVQPGAEREKPGAGEGAGENWEPRVLPYHPAQPGQAACKAVTRYISTELGIRQRLAVL
TSQTTLTPLTGVAVNRTLGHRLERVVFLTGARGRRAPPGMAVVTLGEERPIGHLHLALRHLE
QHGGDDFDWFFLVPDTTYTEAHGLARLTGHLSLASAAHYLGRPDQDFIGGETPGRYCHGGFG
VLLSRMLLQQLRPHLEGCRNDIVSARPDEWLGRCILDATGVGCTGDHEGVHYSHLELSPGEP
VQEGDPHFRSALTAHPVRDPVHMYQLHKAFARAEELERTYQEIQELQWEIQNTSHLAVDGDRA
AAWPVGIPAPSRPASRFEVLRWDFYTEQHAFSCADGSPRCPLRGADRADVADVLGTALELN
RRYHPALRLQKQQLVNGYRRFDFARGMEYTLDLQLEALTPQGRRPLTRRVQLLRPLSRVEI
LPVPYVTEASRLTVLLPLAAERDLAPGFLEAFATALEPGDAAAALTLLLLYEPRQAQVA
HADVFAPVKAHVAELERRFPGARVPWLSVQTAAPSPLRLMDLLSKKHPLDTLFLLAGPDTVL
TPDFLNRCRMHAISGWQAFPPMHQAFYHFGVAPVQGGPPELGRDTRGRFDQAAEACFYNS
DYVAARGRLAAASEEELLESLDYHFLFHFSSHLVLRAVEPALLQRYRAQTCARLSIDL
YHRCLOSLVEGLSRTOLAMLLFEOEGNST

FIGURE 234

GCTCTGGCCGGCCCCGGCGATTGGTCACCGCCCGCTAGGGGACAGCCCTGGCCTCCTCTGAT
 TGGCAAGCGCTGGCCACCTCCCCACACCCCTTGCGAACGCTCCCCTAGTGGAGAAAAGGAGT
 AGCTATTAGCCAATTGGCGAGGGCCCGCTTTTAGAAGCTTGATTTCCTTTGAAGATGAAAG
 ACTAGCGGAAGCTCTGCCTCTTTCCCCAGTGGGCGAGGGAACTCGGGGCGATTGGCTGGGAA
 CTGTATCCACCCAATGTCAACGATTTCTTCCTATGCAGGAAATGAGCAGACCCATCAATAA
 GAAATTTCTCAGCCTGGCCGAAAATGTTGGCCCCACGAAGCCACGACAACTGGAGGCAAAG
 AGGGTTGCTCAACGCCCCGCTCATTTGAAAACCAAATCAGATCTGGGACCTATATAGCGTG
 GCGGAGGCGGGGCGATGATTGTGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTTCT
 TTCCCCGGCCCTGAGACCTTGCAGCACCATCTGT**CATG**GCGGCTGGGCTGTTTGGTTTGAGC
 GCTCGCCGTCTTTTGGCGGCAGCGGCGACGCGAGGGCTCCCGGCCGCCGCTCCGCTGGGA
 ATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCTGTGGCGGGAAGCGGCCCCAGAAC
 CGACCACACCGTGGCAAGAGGACCCAGAACCAGAGACGAAAACCTTGTATGAGAAGAACCCA
 GACTCCCATGGTTATGACAAGGACCCCGTTTTGGACGCTCTGGAACATGCGACTTGTCTTCTT
 CTTTGGCGTCTCCATCATCCTTGGTCCTTGGCAGCACCTTTGTGGCCTATCTGCCTGACTACA
 GGATGAAAGAGTGGTCCCGCCGGAAGCTGAGAGGCTTGTGAAATACCGAGAGGCCAATGGC
 CTTCCCATCATGGAATCCAATGCTTCGACCCAGCAAGATCCAGCTGCCAGAGGATGAG**TG**
ACCAGTTGCTAAGTGGGGCTCAAGAAGCACCGCCTTCCCCACCCCTGCCTGCCATTCTGAC
 CTCTTCTCAGAGCACCTAATTAAAGGGGCTGAAAGTCTGAA

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FIGURE 235

MAAGLFGLSARRLLAAAATRGLPAARVRWESSFSRTVVAPSAVAGKRPPEPTTPWQEDPEPE
DENLYEKNPDSHGYDKDPVLDVWNMRLVFFFGVSIILVLGSTFVAYLPDYRMKEWSRREAER
LVKYREANGLPIMESNCFDPSKIQLPEDE

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FIGURE 236

GGCGGCTGGGCTGTTTGGTTTGAGCGCTCGCCGTCCTTTTGGCGGCAGCGGCGACGCGAGGGC
TCCCGGCCGCCCCGCTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCGCT
GTGGCGGGAAAGCGGCCCCAGAACCGACCACCGTGGCAAGAGGACCCAGAACCCGAGGA
CGAAAACTTGTATGAGAAGAACCAGACTCCCATGGTTATGACAAGGACCCGTTTTGGACG
TCTGGAACATGCGACTTGTCTTCTTCTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACC
TTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCT
TGTGAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAAGTCTTCGACCCAGCA
AGATCCAG

FIGURE 237

GC GGCGCGGTATGCGCGCTTGCTCTGCTCGTCCGTTGCTCTTGGGGCCGCGCGCTGGTGCCT
TGCAGAAACCCCAAGCCGACAGCCTCGGGGAGGAACATGTGCATACCCCGCTGCCCTCCGGG
ACGTAGCCGCGACAGATCCAGTTCGCGACGCGCTGGGAATCGGAGCTTCACGCGGAAGAGATG
TCCCATTCACAGGCTCTTTCCCAAAGCCCTGGGGCAGCTGATCCAAAGTATTCTCTACGGGA
GCTGCACCTGTGCTATTCACAAAGGCTTTTGGAGAACCCGATCGGGGGCCACCCCTCTCTGC
AGGCCCATTCAGTGCAGAGCTGTGGGCTGTGGTTCCAGACACTGCTACTGATGTGGATAAA
TCTTGAAGGAGCTCAGTAATGTCTCTCAGGATCTCTTCCGCGCTCTCTCAACTCTATCGA
CTCCACCAACACAGTCACTCCCACTGCCTCTCTCAAACCCCTGGGTCTGGCAATGACACTG
ACCACTACTTTCTGCGCTATGCTGTGCTGCGGGGAGGTGGTCTGCACCGAAACCTCACC
CCCTGGAAGAAGCTCTTGCCCTGTAGTTTCCAAGGACGCCCTCTCTGCTGCTGAAGGCAGA
TCGCTTGTTTCCACACAGTACCATTCCAGGAGCTGAGGCTGCTGCTGCTGCTTTCGCAAGAT
CACGCTGTACTAGCATCTCCTGGGAGCTGAGGCAGACCTCTGTCAGTTGTATTGTATGCCTTC
ATCACGGGGCAGGGAAGAAGAAGATGCTCCCTCTCCGGATGTTCTCCGACACCTCACGGA
GCCCTGCCCTGGCTCTCAGAGAGCCGAGTCTATGTGGATGATACCACTTCAACCAAGGACA
ACGAGACATTAGAGTGCACCCACCCCGACCATACATACAGGAGCTATCTTAGGCATCT
CGGAAGACCTATGCCATTGACTGATCTTGACACCGCATGATCAACAACCTCTCGAAACCT
CAACATCCAGTCAAGTGAAGAGAGCTCCCGAGAGAATGAGGCCCCCCAGTGCCTCTCTCTGC
TATGCCACGGGTAGCTGAGTGCTATTTGGGCTGCAGAAAGGGGAGCTGAGCACCTGCTGTAC
AACACCCACCATACGGGGCTCTCCCGGCTGCTGCTGCTGCTGACACCGTACCTGGTATCTGCG
GCTGTATGTGCACACCTCACCATCACTCCAAGGGCAAGGAGAACAAACAGTTACATCTC
ACTACAGCCTGCCACAGGACCGGCTGCCAACCCCACTCTCGAGATGCTGATTAGCTGCGG
GCCAATCAGTCACCAAGGTTTCCATTCAGTTTGAAGCGGGCTGCTGAAAGTGACCGAGTA
CACGCCAGATCTTAACATTGCTCTATGTGACCGCATCTGCTCTCAACCGCCCTGTGGCCCA
GCATGGTAGACCAAGGAGTGACTTGGGAAGAGAGTCCCTCTTCAACAGCCTGTGTCCCA
GTCTCTGATGGCTCTAACTACTTTGTGCGGCTCTACACGGAGCGGCTGCTGGTGAACCTGCC
GACACCGGACTCAGCATGGCCCTACAACGTATCTGCCCTACGCTGCACTGTGTTGGCCCTGC
GTACGGCTCTCTTACAATCTCTCAACCGAATCTTCACTCAGGAGAGCCCGCAGAGT
GGCTTGCCCAAGCGCTGGCCAACTTTATCGGCGCGCCGAGGTGTCCCCCACTCTGAAT
CTTGCCCTTTCCAGCAGCTGCAGCTTTCCTCTCTGGGGAGGGGAGCCCAAGGCTGTT
TCTGCGCACTTGCTCTCTCAGAGTTGGCTTTTGAACCAAGTGCCCTGGACCAAGTCAAGGC
CTACAGCTGTGTGTGTCAGTACAGGAGCCAGGAGCAAAATGGGCATTGAAATTTGAAATAA
TCTAGAATAATCTTCTCACTCTGATGTGCCAAGCTCTATATTGAGTGTCTCAATAAAGCAA
AGTGGTTCGGTGGCTGCTGTATTGGACAGCACAGAAAGAGTTCCATCAACACAGAAAGGTC
GGCTGCGCAGCACTGCCAAAGGTGATGGGGTGCTGTCACACAGTGTATGCTCACTGTGTAGTGA
TGAGATTACTGTTTGTGGAATAAAACCGCTGTTTCCGTGGAATAAAAAAAAAA

FIGURE 238

MPLALLVLLLLGPGGWCLAEPPRDSLREELVITPLPSGDVAATFQFRTRWDSSELQREGVSHY
RLFPKALGQLISKYSLRELHLSFTQGFWRTRYWGPPFLQAPSGAELWVWFQDVTVDVDSWK
ELSNVLSGIFCASLNFIDSTNTVTPTASFKPLGLANDTDHYFLRYAVLPREVVCTENLTPWK
KLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCRNARCTSSISWELRQTL SVVFDAFITG
QGKKDWSLFRMFRTLTPECPPLASESRVYVDITTYNQDNETLEVHPPPTTTYQDVILGTRKT
YAIYDLLDTAMINNSRNLNIQLKWKRPPENEAPPVPFLHAQRYVSGYGLQKGELSTLLYNTH
PYRAFPVLLLDTPVWYLRLYVHTLTITSKGKENKPSYIHYQPAQDRLQPHLLEMLIQLPANS
VTKVSIOFERALLKWTEYTPDPNHGFYVSPSVLSALVPSMVAAPVDWEESPLFNSLFPVSD
GSNYFVRLYTEPLLVLNLTPTDFSMYPNVICLTCTVVAVCYGSFYNNLLTRTFHIEEPRTGGLA
KRLANLIRRARGVPFL

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FIGURE 239

CAACATGGGGTCCAGCAGCTTCTTGGTCCTCATGGTGTCTCTCGTTCTTGTGACCCTGGTGG
CTGTGGAAGGAGTTAAAGAGGGTATAGAGAAAGCAGGGGTTTGCCAGCTGACAACGTACGC
TGCTTCAAGTCCGATCCTCCCAAGTGTACACAGACCAGGACTGTCTGGGGGAAAGGAAGTG
TTGTTACCTGCACTGTGGCTTCAAGTGTGTGATTCTGTGAAGGAAGTGAAGAAGGAGGAA
ACAAGGATGAAGATGTGTCAAGGCCATACCCTGAGCCAGGATGGGAGGCCAAGTGTCCAGGC
TCCTCCTCTACCAGGTGTCTCAGAAATGAATGCTGGGTCTTTCTACCTCTGGGGGTCACTC
TCACTTGGCACCTGCCCTGAGGGTCCTGAGACTTGAATATGAAGAAGCAATACCCAACC
CCACCAAAGAAAACCTGAGCTTGAAGTCCTTTTCCCCAAAAGAGGGGAAGAGTCACAAAAAG
TCCAGACCCAGGGACGGTACTTCCCTCTCTACCTGGTGTCTCCTAATGCTCATGAAT
GGACCCCTCATGAATGAAACCAAGTGCCTTATAAGAGACCCCAAAGAGCTGCCTTGCCCTTC
TGCAATGTGTGATCAGCTAGAAGGCACTGTCAGAGAAGAGAACTGGTCTCACCAGATG
CTGAATCTGCTGGTGCCTTGATCTTGACTTCCCAGCCTCTAGAAGTGAAGAAATAAATAT
TTGCTGTTTATAATCCAA

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FIGURE 240

MGSSSFVLVMSLVLTIVAVEGVKEGIEKAGVCPADNVRCFKSDPPQCHTDQDCLGERKCC
YLHCGFKCVIPVKELEEGGNKDEDVSRPYEPFGWEAKCPGSSSTRCPQK

Signal sequence:

amino acids 1-19

N-myristoylation sites:

amino acids 23-29, 27-33, 32-38, 102-108

WAP-type 'four-disulfide core' domain signature:

amino acids 49-63

FIGURE 241

AAACCTCAGCACTTGC CGGAGTGGCTCATTTGTTAAGACAAAGGGTGTGCATCTCTGCCCAGG
AAACCTGAGCGGTGAGGACTCCCGAGTGCCTACATCAGGCCCGCAGGACATGCAGAACCTTCC
TCTAGAACCCTGACCCACCACATGAGGTCTGCTGTGGAGATGCAGGCACCTGAGCCAAAGG
CGTCCAGTGTCTTGTCTTCTGCTGTCTGGTCTTCTTTCTCTTGCCTTGCCTCTTTT
TTAAGGAGGCTCAAAACAAAGCCTTCAGGATCAACGCACAGAGAACATTAAGAAAGGTTCT
CTACAGTCCCTGTGCAAGCGTTAAGTCTCCAGGCCACCAAGAGGAGGAGGACACCTTCTA
TGCAGAGCCAGCGCCAGAGAACATGCCCTCAACACACAAACCCAGGCCCAAGGCCACACCA
CCGGAGACAGAGAAAGGAGGCCAACACCGCCAGGAGGACAGGATGTCCTCCCA
ACAGACAGAGGCGAGATGGAAGAGGCCAGAAAAGAGAAACCTTGGTGAACACACTGTCT
ACCCAGAGGGCAAGATGCAGGGATGGCCTCTGGCAGGACAGAGGCAACATGGAAGAGGC
AGGACACAAAGACGACCAGGAATTTGGGGCCAGACAGGAAGTACGCGCTCCAGAGCG
GTGTGACAGAAAGCACAGGGGCAAAAGCGGCCAACACAGCCAGACGCTCATTTCCCAAAGTCA
GCACAGATGTCTGGCTCCCAAGGACAGTGTCAACAGGACAGAGACAGAAAGGAGGTGACCA
CAGCAGTCACTCCACCTTAAGGAGAAAGAACTCAGGCCACCCACCCCTGGCCTTTCCAG
AGCCCCACGACGCAGAGAAACCAAGACTGAAGGCCGCAACTCAAATCTGAGGCTCCGTG
GGATTTTGAGGAAAAATACAGTCTCGAAATAGGAGGCTCTCAGACGACTTGCCTGACTGT
TGAAGATCAAGGCTCCAGTGCCTGTGGCTCGAGAACTCTTTTGCCAACTTCACTCTC
TTCCTGGACTCCAGACACTCAACACAGATGTGAGTGGGACCGCTGGAACACTTGCACACC
CTTTGGCTTCAAGAGTCAACTACTCTTGGTGCAAGAGTCGTGACAGCTTCCCTCCAG
TGCCCCAGCAGCAGCTGCTCTTGCCAGCCTCCCCGTGGGAGCCTCCGTGTCATCACCTGT
GCCGTGGTGGGCAACGGGGGCTCTGTAACAACTCCCACATGGGCCAGGAGATAGACAGTCA
CGACTAGTGTTCGAGTTGAGCGGAGCTCTATTAAAGCTACGAACAGGATGTGGGACTC
GGACATCCTTCTACGGCTTTACCGCCTTCTCCCTGACCCAGTCACTCTTATATTGGGCACT
CGGGGTTTCAAGAAAGCTGCCTCTGGGAAGGACGTCGCTACTTGCACTCTGGAAGGCAC
CCGGGACTATGAGTGGTGTGGAAGCATGCTTATGAATCAGACGGTGATGCAAAAACCTTT
TCTGGTTCAGGCACAGCCCGGAAGCTTTTCGGGAAGGCCCTGCACATGACAGGTACTGT
TTGCTGCACCCAGACTTCTCCGATACATGAAGACAGGTTTCTGAGTCTTAAGCACTGGA
TGGTGCCACTGGAGGATATACCGCCCCACCATGGGGCCTTCTGCTGCTCACTGCCCTTC
AGCTCTGTGACCAAGTGAGTGTCTATGGCTTCATCACTGAGGCCATGAGCGCTTTCTGAT
CACTACTATGATACATCTGGAAGAGCGCTGATCTTTACATAAACCATGATCTCAAGCTGGA
GAGAGAAGTCTGGAAGCGGTACACGATGAGGGGTAATCCGGCTGTACCAGCGCTCTGGTC
CCGGAATGCCAAAGCCAGAACTGACCGGGGCCAGGGCTGCCATGTCTCTTCTGCTGCTC
CAAGGACAGGATAGCATGGGAATCTTGAGACTTTTGCCATTTCCCTAGGCTCAGACTAA
GCTCCAAGCCCTTCAGGAGTTCAAGGAAGAACTTGAACTGACAGAGCTCTCTCAAGAT
GGCAAAATGGCTAATTGAGGTTCTGAAGTCTTCTAGTACATGCTGAGTCTCTGAGGCCAGG
GATTTTTAATTAATGGGGTGATGGGTGGCCAAATACCAAAATCTGCTGAAAAACACTTT
CAGTCCAAAAGCTCTTGTATACAGAAAAAGAGCTGGATTTACAGAAACATATAGACTGT
GTTTGAATTCCAGTCTGAGTTTACAGTTGTAAGTCTGAAGGTATTACTTAACCTCACTAC
AGATTGTCTAGAAGACCTTTCTAGGAGTTATCTGATTCTAGAAGGGTCTATACTTGTCTTGT
TCTTTAAGCTTTGACAACTCACTGTGTTGTGAGAAACTGATAATAACAAATGATTGT
GTCTATGGAAGGCAAAATAAATTTTCTACAGTGAAAAAATAAAAAA

FIGURE 242

MRSCWLRCRHLSSQGVQWSLLLAVLVFFLFALPSFIKEPQTKPSRHQRTEENIKERSLQSLAKP
 KSQAPTRARRRTTIYAEPA PENNALNTQTQPKAHTTGDRGKEANQAPPEEQDKVPHTAQRAAW
 KSPEKEKTMVNTLS PRGQDAGMASGRTEAQSWSQDQTKTQGGNGQTRKLTASRTVSEKHQG
 KAATAKTALIPKSSQHRMLAPTGA VSTRTRQKGVTTAVIPPKEKKPQATPPAPPFQSPTTQRN
 QRLKAANFKSEPRWDFEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKLFPLNLTFLDSRHF
 NQSEWDRLEHFAPPPFGFME LNYSLVQKVVTFRFPVPQQQLLLASLPAGSLRCITCAVVGNGG
 ILNNSHMGQEIDSHDYVFRLSGALIKGYEQDVGTRTSFYGF TAFSLTQSLLLILGNRGFKNVP
 LGKDVRYLHFLEGRDYEWLEALLMNQTVMSKNLFWFRHRPQEA FREALHMDRYLLLHPDFL
 RYMKNRFLRSKTL DGAHWRIYRPTTGALLLTALQLCDQVSAYGFITEGHERFSDHYIDTSW
 KRLIFYINHDFKLEREVWKRLHDEGIIRLYQRPGPGTAKAKN

Cytoplasmic Domain:

amino acids 1-10

Type II Transmembrane Domain:

amino acids 11-35

Luminal catalytic Domain:

amino acids 36-600

Ribonucleotide Reductase small subunit Signature:

amino acids 481-496

N-glycosylation Sites:

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

FIGURE 243

CGATGCGCGGACCCGGGCACCCCTCCTCCTGGGGCTGCTGCTGGTGGTGGGGCCTTCGCCG
GAGCAGCGAGTGGAATTTGTTCTCGAGATCTGAGGATGAAGGACAAGTTTCTAAACACCT
TACAGGCCCTCTTTATTTTAGTCCAAAGTGCAGCAAACACTTCCATAGACTTTATCACAACA
CCAGAGACTGCACCATTCCTGCATACTATAAAAGATGCGCCAGGCTTCTTACCCGGCTGGCT
GTCAGTCCAGTGTGCATGGAGGATAAGTGAGCAGACCGGTACAGGAGCAGCACACCAGGAGCC
ATGAGAAGTGCCTTGAAACCAACAGGGAACAGAACTATCTTTATACACATCCCCTCATGG
ACAAGAGATTATTTTTGCAGACAGACTCTTCATAAGTCCTTTGAGTTTTGTATGTGTGTG
ACAGTTTGCAGATATATATTCGATAAATCAGTGTACTTGACAGTGTTATCTGTCACTTATTT

CGCGGACCCGGGCACCCCTCCTCCTGGGGCTGCTGCTGGTGGTGGGGCCTTCGCCG

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FIGURE 244

MRGPGHPLLLGLLVLGFSPEQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFRLYHNT
RDCTIPAYYKRCARLLTRLAVSPVCMDK

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FIGURE 245

GGGCTGGGCCCCGCCGACGTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTTCTCTGGGAGG
 CCCGACCCCGGCCGCGCCAGCCCCACCAATGCCACCCGCGGGGCTCCGCCGGGCGCGCCG
 CTCACCGCAATCGCTCTGTTGGTGTGGGGGCTCCCCCTGGTGCTGGCCGGCGAGGACTGCCT
 GTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTTAACTGCGAGTTCTTCACCTTCT
 GCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTATCACCAGAGG
 CAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGCCTCAGCTGTGAT
 CCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTCTGTTGCTACCTGT
 ACCGCCGGCGCCAGCAGCTCCAGAGCCCATTTGAAGGCCAGGAGATTCCAATGACAGGCATC
 CCAGTGACGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGGCCCTGCACCCCCACAGCC
 TGGCTTCATGTACCCACCTAGTGGTCCTGCTCCCCAATATCCACTCTACCCAGCTGGGCCCC
 CAGTCTACAACCCTGCAGCTCCTCCTCCCTATATGCCACCACAGCCCTCTTACCCGGGAGCC
TGAGGAACCAGCCATGTCTCTGCTGCCCCCTTCAGTGATGCCAACCTTGGGAGATGCCCTCAT
 CCTGTACCTGCATCTGGTCCTGGGGGTGGCAGGAGTCTCCAGCCACCAGGCCCCAGACCAA
 GCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCCAGGGAAGTGGAACAGGAGCTGAACTAGA
 ACTATGAGGGGTTGGGGGGAGGGCTTGGAATTATGGGCTATTTTTACTGGGGGCAAGGGAGG
 GAGATGACAGCCTGGGTACAGTGCCCTGTTTTCAAATAGTCCCTCTGCTCCCAAGATCCCAG
 CCAGGAAGGCTGGGGCCCTACTGTTTGTCCCCTCTGGGCTGGGGTGGGGGAGGGAGGAGGT
 TCCGTCAGCAGCTGGCAGTAGCCCTCCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTG
 CTAGATTAAAGCTGTAAAGACAAA

FIGURE 246

MPPAGLRRAAPLTAIALLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCCGTCYHRYC
CRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFLCSCCYLYRRRQQLQSP
FEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYNPAAPPP
YMPPQPSYPGA

Transmembrane Domains:

amino acids 10-28, 85-110

N-glycosylation Site:

amino acids 38-41

N-myristoylation Sites:

amino acids 5-10, 88-93

GGGGAGCTTAGGCCGCGCGCAGTAGTGGTGGCGCGCGCGCAAGGGTGAGGGCGCGCCAGAA
CCCCAGGTAGGTAGTAGCAAGAAAGATGGTGTCTTCTGCCCTCAAAATGGTCCCTTGTCACCACTG
TCTATTCTCATCTTCTCATCTGTGGCTCTTCTTAAGTGTGTCACTCTCTCATGGTGTGCAGAG
CTAGTGAAGCATCTCCAAACGTAGTGTAGGAGACCAATTTCTTGGAAATAAATACGACTCT
CTAGTACGTCTATCCCAAGTCTTATTATGATCTCTGTATCATGTCAAACTTACACGCTGACC
TCTTGGGGAACCCAGCAAGATAGAAATACACAGCAGTACGCCACCAGCCATCATCTGCA
TAGTCAACCACTCGAGATATCTAGGGCCACCTCAGGAAGGGAGCTGGAGAGAGGCTATCTCG
AAGAAGCTCTGCAAGTCTGGAACACCCCTCAGGAGCAAAATGCATCTGTGGCTCCCGAG
CCCCCTCTTGTGGGCTCCCGGTACAGACTGTCTACTATGTGGCAATCTTCTGGAGA
TTTCCACGGATTTCACAAAGCACTTACAGAACCAAGGAAGGGAACTGAGGATACCTAGT
CAACACAATTTGAACCACTCGAGCTAGAAATGGCTTTCTCTTGTATGAACCTCTCTT
AAAGCAAGTTTCTCAATCAAAATTAAGAGAGAGCAAGGCACCTAGCCATCTCTCAATATGCC
ATTGTGTAATCTGTGACTGTGTCTGAAGGACTCATAAGAAACCATTTGTATGTGTGAG
AGATGAGCACTTATCTGTGGCTTCACTCATTTTCAGATTTTGTAGTCTCTCAAGATAAAC
AAGAGTGGAGTCAAGGTTCTGTATTATGTGTGCCAGACAAGATATCTCAAGATTAAC
ACTGGATGCTCGGGTACTCTTCTAGAAATTTATGAGGAGATATACAGATACCGTATCCCC
TACCCAAACAAGATGTCTGCTGCTATCTCGAATTTTGTGTGTGTGTATGGAAGATCTGGA
CTGACAACATATAGAAATCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
GCTTGGCATCAGAGTACTGTGCCCCATGAACGGCCACCACTGTTTGGGAACCTGTGTCA
CTATGGAAATGGTGGAATGATCTTCTTGGCTAAATGAGGAATTTCAAAATTTTGAAGTTTGT
TCTGTTCAGTGTGACCCATCTGAAACATCTGACCACTCTGCTTCTTCTGGCAAACTGTTTGA
CGCAATGGAGGTAGATGCTTAAATTTCTGACACCCCTGTCTTCACTTGTGGAATACCTGT
CTCAGATCGGGAGATGTGTATGATCTTTCTTATGATAAGGAGCTTGTATTTCTGAAATGT
CTAAGGGAGTATCTGAGCGTACGCAATTTAAAGTGTGTTTACAGATCTTCCAGAAAGCA
TAGCTTAAAAAATCAAAAAAGAGGACCTTGGGATAGTATGGCAAGTATTTGCCCTACAG
TATGGTGTAAAAAGGAAGAGTGGCTTTTGTCTAGAAGTCAACATCTATCTTATCTCACAT
TGGCTTACAGAGGAGGAGTGTGTAAGAAACCATGATGAACACTTGGACATGCAAGGGGTTT
TCTCTAAAGTATCATGATCAGTGAAGGGGAGGAATTACACATGAAGCAAGAGCATACATGA
AGGCTCTCAACGCGCCCGGACACTGGGTACCTTGGGCATGTTCATATGACATTCATCAC
AGCAAATCCAACATGGTCCATCGATTTTGTCAAAAAACAAACAGATGTGCTATCTTCCC
AGAAGAGTGGAAATGATCAAAATTAATGTGGGCATGAATGGCTATTACATGTGCTATACG
AGGATGATGATGGGACTTTTTCAGTGGCTTTTAAAGGAACACACACAGCAGTACAGAT
AATGATCGGGCAAGTCTCATTAAACATGCATTTCACTGTGAGCTTGGGAAGTGTCCAT
TGAAGAGGCTTGATTTTCTTATCCTGTACTTGAACATGAACATGAATATTCGCCGTGTTTTC
AAGTTTGAATGAGCTGATCTTATGTATAGTTTATGAAGGAAAGAGATATGAATGAAGT
GAAATCAATTCAGGCCCTTCTCATCAGGCTGTAAGGAGCACTTATGATGAAGCAGATG
GACAGCAGAGGGGCTCAGTCTCAGAGCAAACTGTGCGGAGTGAACATCTACTCTCGCTGT
TGCACAACTCATCGCCGTGCGTACAGAGGGCAGAAGGCTATTTCAGAAAGTGAAGGAATCC
AATGGAAATCTTGAGCTGCCGTGTCGACGTGACCTTGGCAGTGTGTTGCTGTGGGGGCCCCAG
CACAGAAAGGCTGGATTTCTTTATAGTAAATATCAGTTTCTTTGTCCAGTATGAGAAAA
GCCAATATGAAATTTGCCCTCTGCAAGAACCCCAAAATGAAGAAAGCTTCAATGGCTACTAGAT
GAAAGCTTGAAGGAGATAAAAATAAACTCAGGAGTTTCCAACAAATCTTACACTCATTTG
CAGGAACCCAGTAGGATACCACTGGCTGGCAATTTCTGAGGAAAAACTGGAACAAACTTG
TACAAAAGTTTGAACTTGGCTCATCTTCCATAGCCCACTGTAATGGGTACAAACAAATCAA
TCTCTCAAGAAACACCGCTTGAAGAGGTAAAGAGGATCTCAGCTCTTGAAGAAAGATGG
TCTCAGCTCCGTTGTGTCCAACAGCAATTAAGAACATTTGAGAAACATCCGTTGTGAATGG
ATAAGAAATTTGATAAAATCAGAGTGTGGCTGCAAAAGTGAAGAGCTTGAACGATTTCTAA
TCTCTCTTCTGCCCGGTTCTGTATCTCTAATCAACCAATTTTGTGTAGTGTAATTTCAA
ACTAGAGATGGCTGTGTTTGGCTCCAACGGAGATACATTTTCTCCCTCAACTCATTTTGA
CTATCCCTGTGAAAAGAAATAGCTGTAGTTTTCATGAATGGCTTTTTCATGAATGGGTCA
TCGCTACCATGTGTTTGTTCATCACAGGTTGGCCCTGCAACGTAACCCAGTGTGGGT
TCCCTGCCACAGAGAAATAAGTACCTTATCTCTCAAAAAAATAAAAAAATAAAAAA

FIGURE 248

MVFLPLKWSLATMSFLLSSLLALLTVSTPWCQSTEASPKRSDGTPFPWNKIRLPEYVIPVH
 YDLLIHANLTTLTFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPQLQVLE
 HPPQEQIALLAPEPLLVGLPYTVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTA
 ARMAFPFCFDEPAFKASFISIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVMSTYLVA
 FIISDFESVSKITKSGVKVSVYAVPDKINQADYALDAAVTLLEFYEDYFSIPYPLPKQDLAA
 IPDFQSGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVAHLELAHQWFGNLVTMEWWNDL
 WLNEGFAKFMFVSVSVTHPELVGDYFFGKCFDAMEVDALNSSHPVSTFVENPAQIREMFD
 DVSYDKGACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMAICPTDGVKGMDSG
 FCSRSQHSSSSSHWHQEGVDVKMTMMNTWTLQRGFPLITITVRGRNVHMKQEHYMKGSDGAPD
 TGYLWHVPLTFITSKSNMVHRFLKTKTDVLILPEEVEWIKFNVGMNGYYIVHYEDDGWDSL
 TGLLKGTHTAVSSNDRASLINNAFQLVSIKLSIEKALDLSLYLKHETEIMPVFQGLNELIP
 MYKLMKRDMDNEVETQFKAFLIRLLRDLIDKQTTWDEGSVSEQMLRSELLLLACVHNYQPCV
 QRAEYGRKWKESNGNLSLPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSSTEKSQIEFALC
 RTQNKEKLQWLLDESFKGDKIKTQEFQILTLIGRNPVGYPYLAQFLRKNWNKLQVQFELGS
 SSIAHVMVGTNQTSTRLEEVKGFSSSLKENGSQLRCVQQTITETIENIGWMDKNFDFKIR
 VWLQSEKLERM

Signal peptide:

amino acids 1-34

N-glycosylation sites:

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

Neutral zinc metalloproteinases, zinc-binding region signature:

amino acids 350-360

FIGURE 249

CAGCCACAGACGGGT**CATG**AGCGCGGTATTACTGCTGGCCCTCCTGGGGTTTATCCTCCCAC
 TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC
 GACCTACCCCGGCAATGGACCCCTAAGAACACACAGCTGCGACAGCGGCTTGGGGTGCCAGGA
 CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGTCTCTCAAGGGCTGCACGG
 AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATC
 TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT
 TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGG
 AAGGTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACTGTTATGAT
 GGCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC
 CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCCGTGGGTATGACTGAGA
 ACTGCAATAGGAAAAGATTTTCTGACCTGTCATCGGGGACCACCATTATGACACACGGAAC
 TTGGCTCAAGAACCCACTGATTTGGACCACATCGAATACCGAGATGTGCAGGTGGGGCAGGT
 GTGTGAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCTCGGTGGGGACAAAAG
 GCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCCTCCTGGG
 GTGCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG
 CAGCGTTCTGCTGAACCTCCCTCCCTCCTCAAGCTGCCCTGTCCCAGGAGACCGGCAGTGTCT
 CTACCTGTGTGCAGCCCCCTTGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG
 GCGCCCACTCATTGTTATGATGGGTACATTCACTCTCAGGAGGTGGGCTGTCCACCAAAAT
 GAGCATTGAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTGAACCACACAGACAAATCG
 GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCTCCTGCCTCTCAGCATGAGGGAGGT
 GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG
 GTGGGGAGTGGTTTGCCCTTCTGCT**TAA**CTCTATTACCCCCACGATTCTTACCAGTGTCTGA
 CCACCCCACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGACACCAGATTCTTTTC
 CCATTCTGTCCATGAATCATCTTCCACACACAATCATTATATCTACTCACCTAACAGCA
 ACACTGGGGAGAGCCTGGAGCATCCGCACTTGCCTATGGGAGAGGGGACGCTGGAGGAGTG
 GCTGCATGTATCTGATAATACAGACCTGTCTTTCA

FIGURE 250

MSAVLLLLALLGFILPLPGVQALLCQFGTVQHVWVSDLPQWTPKNTSCDSGLGCQDTLMLI
ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPLSLISYTFVCRQEDFCNNLVNSLPLWAPQP
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRRLRGGGIFSNLRVQGCMFQPGCN
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETL
LLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDL CNSASSSVLLN
SLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGVGLALAPALWWGVVC
PSC

FIGURE 251

GCGACGGGCAGGACGCCCCGTTGCGCTAGCGCGTGCTCAGGAGTTGGTGTCTCGCTGCGCT
 CAGG**ATG**AGGGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCCTTCCTGTCACTGCTG
 CCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCTGCTCTGTGCAGATCCTCGTCCCTGG
 CCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCCGACGGCCTGGAAGAGTCG
 GCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGTGTGGGTCTGTAT
 GGAAAAATTGGTCCCATTTGGCTCTAAAGGTGAGAAAGGAGATTCCGGTGACATAGGACCCCC
 TGGTCTTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTGCGCAAGGCCATCGGGG
 AGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTCATCAAGAATGCTGTGCGC
 GGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAGGAGGAGAAGCGCTACGCGGA
 CGCCAGCTGTCTCTGCCAGGGCCGCGGGGACGCTGAGCATGCCAAGGACGAGGCTGCCA
 ATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTGGCCCGTGTCTTCATCGGCATCAAC
 GACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGACCACTCCCCCATGCGGACCTTCAACAA
 GTGGCGCAGCGGTGAGCCCAACAATGCCTACGACGAGGAGACTGCGTGGAGATGGTGGCCT
 CGGGCGGCTGGAACGACGTGGCCTGCCACACCACCATGTACTTTCATGTGTGAGTTTGACAA
 GAGAACATG**TGA**GCCTCAGGCTGGGGCTGCCCATTTGGGGGCCCCACATGTCCCTGCAGGGTT
 GGCAGGGACAGAGCCAGACCATGGTGCCAGCCAGGAGCTGTCCCTCTGTGAAGGGTGGAG
 GCTCACTGAGTAGAGGGCTGTTGTCTAACTGAGAAAAATGGCCTATGCTTAAGAGGAAAATG
 AAAGTGTTCTGGGGTGCTGTCTCTGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCCA
 ATGTCATTATGTAATTATACCCAGAATTGCTCTTCCATAAAGCTTGTGCCTTTGTCCAAGC
 TATACAATAAAATCTTTAAGTAGTGCAGTAGTTAAGTCCAAAAAAAAAAAAAAAAAAAA

MRGNLALVGLISLAFSLSPSGHPQPGADDACSVQILVPLGLKGDAKEGDKGAPGRPRGRVG
PTGEKGMGDKGQKQSGVRHGKIGPITGSGKEKGSDDTGPFGNGEPLGPCESQLRKAIGE
MDNQVSQLTSELFKIKNAVAGRETESKIYLLVKEEKRYADAQLSCQGRGGLTSMPKDEAAN
GLMAAYLAQAGLARVFIGINDLEKEGAFVYSDHFSMRTFNKWRSGEFPNNAIDEEDCVEMVAS
GGWNVDACTHTMYFMCFDKENM

FIGURE 253

AGTGA CTGCAGCCTTCCTAGATCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAG
CACCAGTGTGTGAGGGGAGCAGGCAGCGGTCCTAGCCAGTTCCTTGATCCTGCCAGACCACC
CAGCCCCGGGCACAGAGCTGCTCCACAGGCACCATGAGGATCATGCTGCTATTACAGCCAT
CCTGGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGG
TTCCTGGCGGGGGCCGAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTC
AAAAGCCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAA
GGAATCAACATCTCCCGAGAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGA
GGAGCGTCCAGCCAGAGGAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCTTCGGCCC
CTTCATCCCAATCAGCTTGGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACC
TTTATTAAGACTCTCCTACGGATGTGAATCAAGAGAACGTCCCAGCTTTGGCATCCTCAAGT
ATCCCCCGAGAGCAGAATAGGTACTCCACTTCGGACTCCTGGACTGCATTAGGAAGACCTC
TTTCCCTGTCCCAATCCCAGGTGCGCACGCTCCTGTTACCTTTCTCTTCCCTGTTCTTGT
AACATTCTGTGCTTTGACTCCTTCTCCATCTTTTCTACCTGACCTGGTGTGAAACTGCA
TAGTGAATATCCCCAACCCCAATGGGCATTGACTGTAGAATACCCTAGAGTTCCCTGTAGTGT
CCTACATTA AAAATATAATGTCTCTCTATTCTCAACAATAAAGGATTTTTCATATGAA
AA

FIGURE 254

MRIMLLFTAILAFSLAQSGAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLK
ALSQASTDPKESTSPKSRDMHDFVGLMGKRSVQPEGKTGFFLPSVRVPRPLHPNQLGSTGK
SSLGTEEQRPL

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 36-45

N-myristoylation site.

amino acids 33-39, 59-65

Amidation site.

amino acids 90-94

Leucine zipper pattern.

amino acids 43-65

Tachykinin family signature.

amino acids 86-92

GGCGCTCTCCGGCTGCTCCTATTGAGCTGTCTGCTCGCTGTGCCGCTGTGCCTGCTGTGCC
CGCGCTGTGCGCGCTGCTACCGCGTCTGCTGGACGCGGGAGACGCCAGCGAGTGGTGATTG
GAGCCCTGCGGAGAGCTCAAGCGCCAGCTCTGCCCCAGGAGCCAGGTGCCCCGTGAGTC
CCATAGTTGCTGCAGGAGTGGAGCCATGAGCTGCGTCTTGGTGGTGTATCCCCCTGGGGC
TGCTGTTCTTGGCTGCGGATCCCAAGGCTACCTCCTGCCAACGTCACTCTCTTAGAGGAG
CTGCTCAGCAAAATACCAGACAAACAGTCTCACTCCCGGGTCCGAGAGCCATCCCCAGGGA
GGACAAGGAGGAGATCCTCATGCTGCACAACAAGCTTCGGGGCCAGGTGCAGCCTCAGGCCT
CCAACATGGAGTACATGGTGAGCGCCGGCTCCGGCCGAGAGGCTGGCACCGGGGGTGGGGC
CTGGGCCACCAAGCTGCTCTGTTCCCAAGCCAGCTCTGTTCCCAAGCCAGTGCCTGTGATGG
CTGGCTCAGGGTCTCCTCTGGCAGGGGAGGATCCCGGCTCTGTTCTGTTTGTGTTGTTGTT
TTGAGACAGGGTCTCACTTGCCACTGACGCTGGAGTGCAATGGCACAATCGTCATGCCCTG
AAACCTTAGACTCCCGGGTTAAGCGATCCTGCTTCAGCCTCCCAAGTAGCTGGAACTACAG
GCATGCACCATGTTGCCAGCTAGATTAAATATTTGTGGAGTAGGGGGTCTTGCTACGT
TGCCGAGCTGTGCTTGAAGCTCTAGGCTCAAGAAATCCTCCTGCCTCAGCCTCTCAAAGTG
CTAGGATTATAGGCATGAGTCAACCCTGTCTGGCTCTGGCTCTGTTCTTAACATTCTGCCAA
ACAACACACGTGGGTTCCCTGTGCAGAGCCTGCCTCGTTGCCTTCATGTCACTCTTGGTAGC
TCCACTGGGAACACAGCTCTCAGCCTTTCCCACTGGAGGCAGAGTGGGGAGGGGCCAGGG
CTGGGCTTTGCTGATGCTGATCTCAGCTGTGCCACAGCTAGCTGCACCACCTGACTTCTC
CTTAGCCCGTGTGAGCCTCACTTTCACCTTGGAGAGTCTTCTCTCGGTGGTGGCATGACT
GTGAGATAAGTCGAGGCTGTGAAGGGCCCGGCACAGACTGACCTGCCTCCCCAACCCCTAGG
CTTTGCTAACCGGGAAGGAGCTAACGGTGACAGAAGACAGCCAAGGTCAACCCCTCCGGGT
GATTGTGATGGGTGTTCCAGGTGTGGTTGGGCATGCTGCTACTTGACCCCAAGCTCCAGTG
TGGAAGCTTCTTCTTGGCTGGTTTCCAGAACTACAGAGGAATGGACCACAGTCTTCCAGG
GTCCTCCTCGTCCACCAACCGGGAGCCTCCACCTTGGCCATCCGTGAGCTATGAATGGCTT
TTTAAACAAACCCACGTCCCAGCCTGGGTAACATGGTAAAGCCCCGCTCTCACAAAAATC
CAAGTTAGCCGGGCGATGTGGTGCCAGCACTGTAGTCCACAGTCAGTGGGACTGAGGTGGAG
GTGGAGTGGGGGTTGGGAGCTGGAGGAAGGAGTACGCTTGAGCCTGGGAAGAGCTCGAGGCTGC
AGTGAGCTGAGATTGCACCACTGCACCTCAGCGCTGGGTGACAGAGCAAGCCCTGTCTCAAAA

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FIGURE 256

MSCVLGGVIPLGLLFLVCGSQGYLLPNVTILLEELLSKYQHNEHSRVRRAIPREDKEEILML
HNKLRGQVQPQASNMEYMVSAAGSRRGWHRGWGLGHQPALFPSQLCSPASACDGLRVSSGR
GGSRLCSVLFVCFETGSHSATDAGVQWHNRHALKP

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 27-31, 41-45

N-myristoylation site.

amino acids 126-132, 140-146

Amidation site.

amino acids 85-89

FIGURE 257

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACT**AT**GGG
GTCTGGGCTGCCCTTGTCTCTCTTGACCTCCTTGGCAGCTCACATGGAACAGGGCCGG
GTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCCTATGAGTCCAGC
TTCCCTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCAC
CCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA**TGA**CAGCCATTGAAGCCTG
TGTCTTCTTGGCCCGGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCTGTCTTT
CAGCAGGCCCCCACCCTCCTGAGTGGCAATAAATAAAATTCGGTATGCTG

FIGURE 259

AATTGTATCTGTGAATGTTAAAACAAACGAAATAAAATAGAAGGAAAACTTCTGAGTTT
CAAAAACAACAGACTAGTACTCTAAAGAACTCTTTAAAACAATTAAGTGTAGGATTGCAGT
TATGATTGGATATTATTTAATTCTGTTTCTGATGTGGGGTTCCTCCACTGTGTTCTGTGTGC
TATTAATATTTACCATTGCAGAAGCTTCATTCAGTGTGAAAATGAATGCTTAGTGGATCTG
TGCCCTTTACGCATATGTTACAAATTATCTGGAGTTCCTAATCAATGCAGAGTCCCCCTCCC
CTCCGATTGTTCTAAAT**TAA**TTGAAAGATGTCTGCTGTGGAAAAAGGCATGTATTTAAATCTG
TATGATTCTCAACCATCTTTAGTTGGGAAAGGTCCTTGAAAGCCAATGGAAATACTTTTTTT
TTTTCTTGCACTAATCAAGTGAGTGTTACCTTTTCACTTAGTAGGATGTGTTGTTACGCTA
GTAAATAGAAACCTGTGTTTATTCTCAGGTATTTTAGAAACAACAGCCATCATTTTATTTT
ATGTGTGTGTTCTTGGCTGTATTCATAAATTATATATTTTGGGCTATCAAATATTACTTCAT
TCAATATAAATAACAATAGTAGAAGTTGTTTACTTAGATATGCTTCTAGTTGCATTTTCTC
AGCCTATGTAAGACTACTTTGTTGTAATAGCCTTTGAAATTTACAGTACTGTCTCTCTACTA
TCTTCAGATTACTTGATTCAAATAACCAATTATGTTTGTAATTGATATTAAATAAACCCAGA
ATAAAAGTTCATATCTACCC

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FIGURE 260

MIGYYLILFLMWGSSTVFCVLLIFTIAEASFVENECLVDLCLLRICYKLSGVPNQCRVPLP
SDCSK

Important features:

Signal peptide:

amino acids 1-29

0990444.11401

FIGURE 261

GAGGATTTGCCACAGCAGCGGATAGAGCAGGAGAGCACCACGGAGCCCTTGAGACATCCTT
 GAGAAGAGCCACAGCATAAGAGACTGCCCTGCTTGGTGTGTTTGCAGGATGATGGTGGCCCTT
 CGAGGAGCTTCTGCATTGCTGGTTCGTTCCTTGCAGCTTTTCTGCCCCCGCCGCTGTGAC
 CCAGGACCCAGCCATGGTGATTACATCTACCAGCGCTTTCGAGTCTTGGAGCAAGGGCTGG
 AAAAAATGTACCAAGCAACGAGGGGCATACATTCAAGAATTCGAAGAGTCTCAAAAAATATA
 TCTGTCTGCTGCGGAAGATGTCAGACCTACACAAGTGAGTACAAGAGTGCAGTGGGTAACTT
 GGCAGTGAAGATTGAACGTGCCAACGGGAGATTGACTACATACAACTCTCGAGAGGCTG
 ACGAGTGCATCGTATCAGAGGACAAGACACTGGCAGAAATGTTGCTCCAAGAAGCTGAAGAA
 GAGAAAAAGATCCGACTCTGCTGAATGCAAGCTGTGACAACATGCTGATGGGCATAAAGTC
 TTTGAAAATAGTGAAGAAGATGATGGACACACATGGCTCTTGGATGAAGATGCTGTCTATA
 ACTCTCCAAAGGTGACTTATTAAATGGATCCAGAAACAACACTGTTTGGGAATTTGCAAAC
 ATACGGGCATTCATGGAGGATAACACCAAGCAGCTCCCCGGAAGCAAATCCTAACACTTTC
 CTGGCAGGGAACAGGCCAAGTGATCTACAAAGGTTTTCTATTTTTTATAACCAAGCAACTT
 CTAATGAGATAATCAAATATAACCTCGACAAGAGGACTGTGGAAGATCGAATGCTGCTCCCA
 GGAGGGGTAGGCCGAGCATTGGTTTTACCAGCACTCCCCCTCAACTTACATTGACCTGGCTGT
 GGATGAGCATGGGCTCTGGGCCATCCACTCTGGGCCAGGCACCCATAGCCATTGGTCTCA
 CAAAGATTGAGCCGGGCACACTGGGAGTGGAGCAATTCATGGGATACCCCATGCAGAAGCCAG
 GATGCTGAAGCCTCATTCTCTGTGTGGGGTCTCTATGTGGTCTACAGTACTGGGGGCCA
 GGGCCCTCATCGCATCAAGCTGCATCTATGATCCACTGGGCATATCAGTGAGGAGGACTTGC
 CCAACTTGTCTTCCCCAAGAGACCAAGAAGTCACTCCATGATCCATTACAACCCAGAGAT
 AAGCAGCTCTATGCTTGAATGAAGGAAACAGATCATTTACAAACTCCAGACAAAGAGAAA
 GCTGCCCTCTGAAGTAAATGCATTACAGCTGTGAGAAAGAGCACTGTGGCTTGGCAGCTGTT
 TACAGGACAGTGAGGCTATAGCCCTTCACAATATAGTATCCCTCTAATCACACAGGAAG
 AGTGTGTAGAAGTGGAAATACGTATGCCCTCTTTCCCAAAATGTCACTGCCTTAGGTATCTTC
 CAAGAGCTTAGATGAGAGCATATCATCAGGAAAGTTTCAACAATGTCCATTACTCCCCAAA
 CCTCCTGGCTCTCAAGSATGACCACATTCTGATACAGCCTACTTCAAGCCTTTTGTGTTTACT
 GCTCCCCAGCAATTAACGTAACTCTGCCATCTTCCCTCCCAAAATAGAGTTGTATGCCAGC
 CCTAATATTCAACTGGCTTTTCTCTCCCTGGCCTTGTGTAAGCTCTTCCCTCTTTTT
 CAAATGTCTATTGATATTCTCCCATTTTCACTGCCCAACTAAAATACTATTAATATTTCTTT
 CTTTTCTTTCTTTTTTTTGGAGCAAGGTCTCACTATGTTGCCAGGCTGGTCTCAAACTCC
 AGAGCTCAAGAGATCCTCCTGCCTCAGCCTCCTAAGTACCTGGGATTACAGGCATGTGCCAC
 CACACCTGGCTTAAATACTATTTCTATTGAGGTTTAACTCTATTTCCCTAGCCCTGTC
 CTCTCCACTAAGCTTGGTAGATGTAATAATAAAGTGAAAATATTAACATTGAATATCGCCAC
 CTAGGTTGGAGTGTGTTGCACATCATGAAATCTCGTTTACCTTTTGTGAACATGCACAAG
 TCTTTACAGCTGTCTATCTAGTCTTAGTGTAGTAAACAAATACAAAGTGAAGATACAGC
 TAGAAAAATCTACAAATCCCATAGTTTTTCCATTGCCCCAAGGAAGCATCAAAATACGTATGT
 TGTTCACCTACTCTTATAGTCAATGCGTTCATCGTTTTCAGCTCAAAATATAGTCTGTGCC
 TTTAGCCAGTTTTTCATGCTGCACAAGACCTTTCAATAGGCCTTTCAAATGATAATTCCTCC
 AGAAAAACAGTCTAAGGGTGAGGACCCCAACTCTAGCCTCCTCTGTCTGTCTGCTCTGT
 TTCTCTCTTTCTGCTTTAAATTCAATAAAAGTGACACTGAGCAAAAAAAAAAAAAA

MMVALRGASALLVFLAAFLPPQCTQDPAMVHYIYQRFVLEQGLEKCTQATRAYIQEFQE
FSKNISVMLGRCTYTSEYKSAVGNLALVERAQREIDYIQYLREADECIVSEDKTLAEMLL
QEAEEEKKIRITLLNASCDNMLGKSLKIVKKMMDTHGSWMKDAVNSPKVYLLIGSRNNTV
WEFANIRAFMEDNTKPAPRKQILITLSWQGTQGVYKGLFFHNQATSNEIIKYNLQKRTVED
RMLLPGGVGRALVYQHS PSTYIDLAVDEHGLWAIHSGPGTHSHLVLTKEIPGTLGVEHSWDT
PCRSQDAEASFLLCGVLYVVYSTGGQGPHRITCIYDPLGTISEEDLPNLFPPKRPRSHSMIH
YNPRDKOLYAWNEGNIQIIYKLQTKRKLPLK

FIGURE 264

MELSQMSELMGLSVLLGLLALMATAAVARGWLRAGEERSGRPACQKANGFPDPKSSGSKKQK
QYQIRIRKEKPQQHNFTHRLAAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSTKDFLQ
REHRSMRANVELDHATLVRFPDCRAFIWLVLANGDTLRVFKMTKREDGGYTFATPEDFPKK
HKAPVIDIGIANTGKFIMTASSDPTVLIWLSLKGQVLSTINTNQMNTHAAVSPCGRFVASCG
FTPDVKVWEVCFGKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKDGTWKLWDTDV
EYKKKQDPYLLKTGRFEEAAGAAPCRLALSPNAQVLALASGSSIHLYNTRRGEKEECFERVH
GECIANLSFDITGRFLASCGDRAVRLFHNTPGHRAMVEEMQGHLKRASNESTRQLQQQLTQ
AQETLKSLGALKK

Important features:**Signal peptide:**

amino acids 1-25

N-glycosylation site.

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

Beta-transducin family Trp-Asp repeat protein.

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

FIGURE 265

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGG
 CAGTGTTTTGCCTTCACCCCAAGTGACC**ATG**AGAGGTGCCACGCGAGTCTCAATCATGCTCC
 TCCTAGTAACGTGTCTGACTGTGCTGTGATCACAGGGGCTGTGAGCGGGATGTCCAGTGT
 GGGGCAGGCACCTGCTGTGCCATCAGCCTGTGGCTTCGAGGGCTGCGGATGTGACCCCGCT
 GGGGCGGGAAGGCGAGGAGTGCCACCCCGGCAGCCACAAGGTCCCTTCTTCAGGAAACGCA
 AGCACCACACCTGTCCTTGCTTGCCCAACCTGCTGTGCTCCAGGTTCCCGGACGGCAGGTAC
 CGCTGCTCCATGGACTTGAAGAACATCAATTTT**TAG**CGCTTGCTGGTCTCAGGATACCCA
 CCATCCTTTTCTGAGCACAGCCTGGATTTTATTCTGCCATGAAACCCAGCTCCCATGAC
 TCTCCAGTCCCTACACTGACTACCTGATCTCTCTGTCTAGTACGCACATATGCACACAG
 GCAGACATACCTCCCATCATGACATGGTCCCCAGGCTGGCCTGAGGATGTACAGCTTGAGG
 CTGTGGTGTGAAAGGTGGCCAGCCTGGTTCTCTTCCCTGCTCAGGCTGCCAGAGAGGTGGTA
 AATGGCAGAAAGGACATTCCCTCTCCCTCCCGAGGTGACCTGCTCTCTTTCTGGGCCCTG
 CCCCTCTCCCCACATGTATCCCTCGGTCTGAATTAGACATTCCTGGGCACAGGCTCTTGGGT
 GCATTGCTCAGAGTCCCAGGTCTGGCCTGACCTCAGGCCCTTCACGTGAGGTCTGTGAGG
 ACCAATTTGTGGGTAGTTCATCTTCCCTCGATTGGTTAACTCCTTAGTTTCAGACCACAGAC
 TCAAGATTGGCTCTTCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGGAGCCCA
 GGGAGGCCAATCAGCCCCCTGAAGACTCTGGTCCCAGTCAGCCTGTGGCTTGTGGCCTGTGA
 CCTGTGACCTTCTGCCAGAATTGTCATGCCTCTGAGGCCCTCTTACCACACTTTACCAGT
 TAACCACTGAAGCCCCAATTCCACAGCTTTTCCATTAAATGCAATGGTGGTGGTTCAA
 TCTAATCTGATATTGACATATTAGAGGCAATTAGGGTGTTCCTTAAACAACCTCCTTTCCA
 AGGATCAGCCCTGAGAGCAGGTGGTGACTTTGAGGAGGGCAGTCCTCTGTCCAGATTGGGG
 TGGGAGCAAGGGACAGGAGCAGGGCAGGGGCTGAAAGGGGCACTGATTACAGACCAGGGAGG
 CAACTACACACCAACATGCTGGCTTTAGAATAAAAGCACCAACTGAAAAA

FIGURE 266

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGECHP
GSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site:

amino acids 88-95

N-myristoylation sites:

amino acids 33-39, 35-41, 46-52

FIGURE 267

AGCGCCCGGGCGTCGGGGCGGTAAAAGGCCGGCAGAAGGGAGGCACTTGAGAAATGTCCTTTCTCCAGGACCCAAAGTTTCTTCACCATGGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGGCTGCTGCCTTGGCATTGCTGCTTGCCAACACAGACGTGTTCTGTGCCAAGCCCCAGAAAGCGGCCCTGGAGTACCTGGAGGATATAGACCTGAAAACACTGGAGAAGGAACCAAGGACTTTCAAAGCAAAGGAGCTATGGGAAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTTTCTCTGTGTCGAGAGGAAGCTGCGGATCTGTCTCCTGAAAAGCATGTTGGACCAGCTGGGCGTCCCCCTCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTTCCAGCCTTATTCAAAGGAGAAATCTTCTGGATGAAAAGAAAAAGTTCTATGGTCCACAAAGGCGGAAGATGATGTTTATGGGATTTATCCGCTCTGGGAGTGTGGTACAACCTTCTCCGAGCCTGGAACGGAGGCTTCTCTGGAACCTGGAAGGAGAAGGCTTCATCCTTGGGGGAGTTTTCTGTGTGGGATCAGGAAAGCAGGGCATTCTTCTTGAGCACCAGAAAAAGAAATTTGGAGACAAAGTAAACCTACTTTCTGTCTGGAAGCTGCTAAGATGATCAAACCACAGACTTTGGCCTCAGAGAAAAATGATGTGTGAAACTGCCAGCTCAGGGATAACCAGGGACATTACCTGTGTTTCATGGGATGTATTGTTTCCACTCGTGTCCCTAAGGAGTGAGAAACCCATTATATACTCTACTCTCAGTATGGATTATTAATGTATTTTAATATTCTGTTTAGGCCCACTAAGGCCAAATAGCCCCAAAACAAGACTGACAAAAATCTGAAAACTAATGAGGATTATTAAGCTAAAACCTGGGAAATAGGAGGCTTAAATTGACTGCCAGGCTGGGTGCAGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCCAAGGTGAGCAAGTCACTTGAGGTCGGGAGTTCGAGACCAGCCTGAGCAACATGGCGAAACCCCGTCTACTAAAAATACAAAAATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCCAGCTACCCGGAGGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGTGGAGGTTGCGGTGAGCTGAGATCACCACTGTATTCCAGCCTGGGTGACTGAGACTCTAACTAA

FIGURE 268

MSFLQDPSFFTGMWSIGAGALGAAALALLANTDVFLSKPQKALEYLEDIDLKTEKEPR
TFKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDF
QPYFKGEIFLDEKKKFYGPQRRKMMFMGFIRLGVWYNFFRAWNGGFSGNLEGEFILGGVFV
VGSGKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

T0111-1110660

FIGURE 269

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCCG
GGCCAGGTGCCCCGTGCGAGGTGCCCCCTGGCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGA
AGCCCCCTTCCTCGGCGCTGCCAACC CGCCACCCAGCCCCATGGGCGAACCCCGGGCTGGGGCTG
CTTCTGGCGCTGGGCTGCCGTTCTTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACA
GACCACCTCTGCAAATGAGAAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATG
GCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGCTGCCTTG
CTCCTGGCTGTGGGGCTGGCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGG
CACCTACCGCCCCAGTAGCGAGGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGG
ACTCCAAGGAGACGGTGCGAGGGCTGCCTGCCCATCTAGGTCCCCCTCTCCTGCATCTGTCTCC
CTTCATTGCTGTGTGACCTTGGGGAAAGGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAG
TGCTTAATAGCAGGGAAGAAGGTACTTCAAAGACTCTGCCCCTGAGGTCAAGAGAGGATGGG
GCTATTCACTTTTATATATTTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAAAAA

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FIGURE 270

MANPGLGLLLALGLPFLLARWGRAWGQIQTTSANENSTVLPSTSSSSDGNLRPEAITAIIV
VFSLLAALLLAVGLALLVRKLEKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

10411 1110660

FIGURE 271

AATATATCATCTATTTATCATTAAATCAATAATGTATTCTTTTATTCCAATAACATTTGGGTT
TTGGGATTTTAAATTTCAAACACAGCAGAAATGACATTTTTCTGTCACATATTATTATGTG
GTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCT
ATCAAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTC
CTACCAAGCTGTCAAACACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGA
GGGTTAATTCCTGGTGCTGAAGCCTGGGGCAGGGGTGTAAAGAAAAACACTTAGATTCAATG
ATTGTAAATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAAATGTATCCCTGTCATA
TATACAATAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGACAGTTCTAAATTGGACT
TTATTAATTTTTAAATCAGTAACTGATTTATCACTGGCTATGTGCTTAGATCTACAGGAGA
TCATATAATTTGATACAAATAAAAGAAAAGTGTCTCTCCCTTACAGAATTGACATTTTAA
ATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAA
AGAAGGGAAATGTTGCCAAGGAAAAAAAAA

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FIGURE 272

MTFFLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGK
GIVKGRNLDSRGLILGAEAWGRGVKKNT

009014-1449

[illegible]

FIGURE 274

MGLFRGQVFLVLLCLLHQSNSTFIKLNNGFEDIVIVIDPSVPEDEKIIIEQIEDMVTASTY
 LFEATEKRRFFKNVSIILPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTKQFTEC
 GEKGEYIHFPTDLLLGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATR
 CSAGISGRNRVYKCQGGSCLSRACRIDSTTKLYGKDCQFFPDQVTEKASIMFMQSIDSVVE
 FCNEKTHNQEAPSLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPPVFSLKISQRIVCLV
 LDKSGSMGGKDRNLNRMNQAAKHFLQTVENGSWVGMVHFDSTATIVNKLIIQIKSSDERNTLM
 AGLPTYPLGGTSICSGIKYAFQVIGELHSQLDGSEVLLLTGDEDNTASSCIDEVKQSGAIVH
 FIALGRADEAVIEMSKI TGGSHFYVSDEAQNGLIDAFGALTSGNTDLSQKSLQLESKGLT
 LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPPSISLWDPSTIMENFTVDATSKMAYLSIPG
 TAKVGTWAYNLQAKANPETLTITVTSRAANSSVPPITVNAKMNDVNSFFSPMIVYAEILQG
 YVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNDDGVYSRYFTAYTENGRYSLKVRAGH
 GANTARLKLRLPLNRAAYIPGWVNGEIEANPPRPEIDEDTQTTLDEDFSRASGGAFFVVSQV
 PSLPLPDQYPPSQITDL DATVHEDKII LTWTAPGDNFDVGKVQRYIIRISASILDLRDSFDD
 ALQVNTTDLSPKEANSKESFAFKPENISEENATHIFIAIKSIDKSNLTSKVSNNIAQVTLFIP
 QANPDDIDPTPTPTPTPTPKSHNSGVNISTLVLSVIGSVVIVNFILSTTI

Signal peptide:

amino acids 1-21

Putative transmembrane domains:

amino acids 284-300, 617-633

Leucine zipper pattern.

amino acids 469-491, 476-498

N-glycosylation site.amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

CTCCTTAGGTGGAAACCTCGGGGATAGAGTACTGACAGCAAAGACCGGGAAGACCATACGTCCCCG
GGCAGCGGCTGACAAACAGGTGTCACTCTTTTGTATCTCGTGTGGCTGGCTCTCTTCTTACAGAAAG
ACCGCAAGGTAATTTTGACCGAGGAGCAATGTGCTACTCAACCAAGACGGCGCTCTCGGCTTAACCT
CCGAGTTTGGACAGGATTTTCTGTGTGGCGTGCCTTCTCTTACGATGCTCAGAAGTAGCTTGGCTGTA
GGGTGGTGGACAGCAAGAAAGGAAGCTCCCTCTGTCTGTGGCTGCATCAGGAAGGCTGTGTATGGG
GTGAGAGCTGAAATCTTGGAGATTTCACTTCCGATATGCTTCTGCTCGCAAGATCATCTTTAAAA
CAAGCAGCTCCGGGGGCCCAAACGCATGCTTCTGTGGTACGCCAGGGAAGCCCTTCGTGGGG
GCCCGCGCTTTGGGGATGACCCGGTTCTGGACGCATGGCTGATCTCTGATGATGATGTTCGCG
GGGGGCTGCTTTGGCTGGATTTCCCGGTGTGGTTTTCGTGTGCTCTCTCTGTGTCTATCTCTGT
CCCTGATCATTTGGCCTGCACCCAAAGGTGACGAGGAGCGATGCGCATGCCAGGGGCCCAACG
CCCACGGGGAAGGAGGGGTAACAGCGCTCTCTCAGGAGTGGGAGGAGCAGCCGCACTCTGAGAA
GACGCTTGAAGCGGCAGATCGCAGCTCAAGGAGGAGCTGCAGGAGGAGGAGGAGGAGGAGGAGAA
TGGCAGATCAACCAAGCAGCGATGCTGCTGGCCTGGGTTCTGCAGCAGAGGAGGAGGAGGAGGAG
GCCGACCTCTGGCCTTCTGCGCATCTGCGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
CCACAGAGTAGTCAGCAGTGGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
CCTTAGCCCGGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
GAG
CTGATTTCTAAGAGGATCTTACCAAGCAGAAAGGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
AGGAGGCCAACAAACGAATTAACAGGCTCATCTTATTGCAACATTGACGCCATTGAAAGATG
AAAAATGAAAGAGCTCAACATGGCCAAACGCTTATCAATGTATTCTGTCGCTCTATGAAACAAAGGTGG
ACAGGTTCCCGCAGTTCTATCGAATTTTCCGGGAGATGTGCATTGACGAGGATGGGAGAGTCCATCT
CACTGTGTGTTTACTTTGGGAAAGAGAATAATTAAGTCAAGGAAGATATCTGAAACACATCTCCAA
GCTGCGCAACTTCAGGAATTTTACCTTTCTATCGACGTGAATGAGAATTTTCTCGGGGAAAGGATCT
ATGTTGGAGGCGCGCTTCTGGAAGGGAAGCAACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
CACATCTGAATTTCTCAATACGTTGAGGCTGAATCGAGCTTGTATGTCAGTCCCTCTCTTGGAAACG
CTTTTTCAGTCAGTACAATCTCGGCATATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
AGCTGTGCTATAAGAGGAATTTGCTGTCT
CTGACAGCT
CT
TCTGCGATGCAAGGCGCTGCTGAGCAGGCTGACCCCGGACGATCAAGATGTGTCATGTCAGTCCAA
GCCGATCAAGCAGCATCCACGCCGCGCTGGGCATGCTGTGTTCTGAGGCACGAGATAGAGGCTCAC
CTTCCGAACAGAAACAGACAGCAGTAGTACGAAAAAACATGAACTCCGACAGAGAAGATTTGTGGGAG
CACTTTTCTTCTCTTTTGAATTAATCGAAGGTGGCTGCACAGAGAAAGACGTTCCATATAAGGAGC
AACAAGAAATTTGGACTGATGGTGCAGAGTAGAAGAAGCTCCGATTTCTCTCTTGTGGCCTTTCTAC
AACAGAAATCAAAATTCGCGTTTTCGCTGCAAAAGTAACCCAGTGTGACCCCTGTGAAGTTCTCTCT
AAGGCAGAAATCGTTGTGAGATTTAAGGCTAATGTTGTGGAGGCTGAGGAGGAGGAGGAGGAGGAG
GAGACCTGTGTTTGTGTGCTCATGAAATTTCTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
TAGCATGAAAGGCAAGCTATCT
AATGCTGAAATTTCT
AATGCTGAAATTTCT
GCATTTTTCCTCTGTGATTTATAGTCTGCTTTATTAATTACCATTTCGAAGCCTTCAAGAGA
GCACAAAGTTGGCTCATTTTTATTTTTTAAAGAGTACTTTGAGATGCATTTAGAAACTTTTCA
GTTCAAGCATCAAAATTTGATGCCATTTCAAGGACATGCCAAATCGCATTTCTGTACGAGCATGAAT
FTCAGGCTATTGAGCATAGGAGGAAGTATGTTTACTAATACAGCTGACAGATCTCTCTCTGAA
TGAATTTTCT
GAGTATTTCT
AAGGAACTTTCTCAGACTGGTATCTGATCTGATGTTACTTAAAGTCAAGTCAAGTCAAGTCAAGT
GAAGTAGGGACCGCTTTCTACCTGTCTTAAATAATGAGTCAAGTCAAGTCAAGTCAAGTCAAGT
TTTCAAAACAGGCTGCT
AT
CT
CCAGATGCTCTGAAATTTGATTTTATTTACCATTTCAACTATTTTAAAAATTAATACAGTTA
ACATAGAGTGGTGTCTATCTTCAATGTAAGTATTATGGCAGCACAGATGATGAGCTAAATTTATCT
CTTTGAGTCTTGTCTTCTGTTTGTCTCAGATAACTCATTTGATTTAAAGCTTCAAGAACCTTCAAG
TGTGTGGTGTGTTAAAAATGCAATGATGATGATTTGTATCTGGTAGTTTGTAAATTTTATTAACAC
AGGCATGAATGGAAGGTGATTTCACAGCAATAAAATATGATTTGTGGATGATGAA

FIGURE 276

MMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQLALPRANSP TGKEGYQAVLQ
EWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGDRSPPEKTQADLLAFL
HSQVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVRKDKRDELVEAIES
ALETLNNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSP
MKVKNELNMANTLINVIVPLAKRVDFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVK
GILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTR
LNTQPGKKVFYPVLFSQYNPGIITYGHDAVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFI
NIGGFDLDIKGWGGEDVHLYRKYLSNLIVVRTPVRLFHLWHEKRCMDELTPEQYKMCMQS
KAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSSKKT

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FIGURE 277

GAAAGAAATGTTGTGGCTGCTCTTTTTTCTGGTGA CTGCCATT CATGCTGA ACTCTGTCAACC
 AGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCAT
 ATGCTCGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA
 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGT
 ATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCTGTGTTGAGGTGC
 AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAAT
 CTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTG
 GATTATTATATTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTAT
 CAGGGATCTGGCAACGTAGAAGAAAGACAAAGAACCATCTGAAGTGGATGACGCTGAAGAT
 AAGTGTGAAAACATGATCACAAATGAAAATGGCATCCCCCTGATCCCCCTGGACATGAAGGG
 GGGCATATTAATGATGCCTTCATGA CAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGT
 TGTTCGTCTCTCTCAAGAAATTAACATTTGTTTCTGTGTGACTGCTGAGCATCCTGAAATA
 CCAAGAGCAGATCATATATTTTGTTCACCATTCCTCTTTTGTATAAAATTTTGAATGTGCT
 TGAAAGTGAAAAGCAATCAATTATACCCACCAACACCACTGAAATCATAGCTATTCACGAC
 TCAAAATATTCTAAAATATTTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTTG
 TAGTTATTGATTTAAGCATTTTTAGAAATAAGATCAGGCATATGTATATATTTTCACACTTC
 AAAGACCTAAGGAAAAATAAATTTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCAT
 TGAAAATGGATCCTTTTTTGACGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAG
 TGAGAAGTAATTATTGTAAATGGATGGATAAAAAATGGAATTACTCATATACAGGGTGAATT
 TTATCCTGTTATCACACCAACAGTTGATTATATATTTTCTGAATATCAGCCCCAATAGGAC
 AATTCTATTTGTTGACCATTTCTACAATTTGTAAAGTCCAATCTGTGCTAACTTAATAAAG
 TAATAATCATCTCTTTTTAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 278

MLWLLFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVP
NREATEISHVLLCNVTQRVSFWFVVTDP SKNHTLPAVEVQSAIRMNKNRINNAFFLNDQTL E
FLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRRKNEPSEVDDAEDKC
ENMITIENGIPSDPLDMKGGILMMPS

EDHFF"HH0660

AAC TCAAACTCCTCTCTCTGGGAAACGCGGTGCTTGCTCCTCCGGAGTGGCCTTGGCAGG
GTGTTGGAGCCCTCGGTCTGCCCGCTCGGTCTCTGGGGCAAGGCTGGGTTTCCCTC**ATGT**
ATGGCAAGAGCTCTACTCGTGCGETGCTTCTTCTCCTTGGCATAACAGCTACAGCTCTTTGG
CCTATAGCAGCTGTGGAAATTTATACCTCCCGGTGCTGGAGGCTGTTAATGGGACAGATGC
TCGGTAAAAATGCACCTTTCTCCAGCTTTGCCCGCTGTGGGTGATGCTCTAACAGTGACCTGGA
ATTTTCGTCTCTAGACGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCTTC
CAACCCATGAGTGGGCGGTTTAAAGACCGGTGCTCTGGGATGGGAATCCTGAGCGGTACGA
TGCTCCATCCTTCTCTGGAACTGCAGTTCGACGACAATGGGACATACACCTGCCAGGTGA
AGAACCACCTGATGTTGATGGGGTGATAGGGGAGATCCGGCTCAGCTGCTGTCACACTGTA
CGCTTCTCTGAGATGCATCTCTGGCTTGCECCATTTGGCTCTGCCTGATGATGATGATCAT
ATAAGTAATTGTAGTGGTCCCTCTTCAGCATATACCGGAAAAAGCGATGGGCCGAAAGAGCTC
ATAAAGTGGTGAGATAAAATCAAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGTCTCT
GTTTATTATTAGAAGACACAGACT**TAA**CAATTTTAGATGGAAGCTGAGATGATTTCCAAGAACAA
GAACCCTAGTATTTCTTGAAGTTAATGGAAACTTTTCTTTGGCTTTTCCAGTTGTGACCCGT
TTTCCAACCAAGTCTGCGAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCAC
AGTGCTCTCCATATCACCAGTCATACACAGCCTCATTATTAAGGTCTTATTTAATTTTCA
GTGTAATATTTTCAAGTGCTCATTAGGTTTTATAAACAAGAAGCTACATTTTGGCCCTTAA
GACACTACTTACAGTGTTATGACTTGTATACACATATATTTGGTATCAAAGGGGATAAAAGCC
AATTTGTCTGTTACATTTCTTTTCACGTATTTCTTTTAGCAGCACTTCTGCTACTAAAGTTA
ATGTGTTTACTCTCTTCTTCCACATTTCTCAATTAAGGTTAGCTAAGCCTCCTCGGTG
TTTCTGATTAAACAGTAAATCCTAAATTCAACTGTTAAATGACATTTTATTTTATGTCTC
TCCTTAACATAGAGACACATCTGTTTCTTACTGAATTTCTTCAATATCCAGGTGATAGATT
TTTGTCG

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FIGURE 280

MYGKSSTRAVLLLLLGIQLTALWPIAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTVT
WNFRPLDGGPEQFVFYYHIDPFQPMGRFKDRVSWDGNPERYDASILLWKLQFDDNGTYTCQ
VKNPPDVGVIGEIRLSVVHTVRFSEIHFLALATGSACALMIIIVVVVLFQHYRKKRWAER
AHKVVEIKSKEERLNQEKKSVMLEDTD

0990111-11402

FIGURE 281

GCATTTTGTCTGTGCTCCCTGATCTTCAGGTCACCACCATGAAGTTCTTAGCAGTCCTGGT
ACTCTTGGGAGTTTCCATCTTTCTGGTCTCTGCCCAGAATCCGACAACAGCTGCTCCAGCTG
ACACGTATCCAGCTACTGGTCCTGCTGATGATGAAGCCCCCTGATGCTGAAACCACTGCTGCT
GCAACCACTGCGACCACTGCTGCTCCTACCACTGCAACCACCGCTGCTTCTACCACTGCTCG
TAAAGACATTCCAGTTTACCCTAAATGGGTGGGGATCTCCCGAATGGTAGAGTGTGTCCCT
GAGATGGAATCAGCTTGAGTCTTCTGCAATTGGTCACAACATTTCATGCTTCTGTGATTTT
ATCCAACTACTTACCTTGCCTACGATATCCCCTTTATCTCTAATCAGTTTATTTCTTTCAA
ATAAAAAATAACTATGAGCAACATAAAAAAAAAAAAAA

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FIGURE 282

MKFLAVLVLLGVSI FLVSAQNPTTAAPADTYPATGPADDEAPDAETTAAATTATTAAPTAT
TAASTTARKDIPVLPKWVGDL PNGRVCP

0990441-11431

FIGURE 283

GGACTCTGAAGGTCCCAAGCAGCTGCTGAGGCCCCCAAGGAAGTGGTTCCAACCTTGGACCC
CTAGGGGTCTGGATTTGCTGGTTAACAAGATAACCTGAGGGCAGGACCCCATAGGGGAATGC
TACCTCCTGCCCTTCCACCTGCCCTGGTGTTCACGGTGGCCTGGTCCCTCCTTGCCGAGAGA
GTGTCTCTGGGTCAGGGACGCAGAGGACGCTCACAGACTCCAGCCCTTTGTTACCGAGAGGAC
ACTTGGCAAGGTCCAGCGATGGTCCGGAGTCCACACACAGACTGGCGGCAGGGCAGGAGGGG
GACAGTTCTGTTGTGCTTGGTTGGACAGTAAGAGGGTCTTGCCAGTCCAGGGTGGGGGGCG
GCAAACTCCATAAAGAACCAGAGGGTCTGGGCCCCGGCCACAGAGTCATCTGCCAGCTCCT
CTGCTGCTGGCCAGTGGGAGTGGCACGAGGTGGGGCTTTGTGCCAGTAAAAACCACAGGCTGG
ATTTGCCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTTGTCTCAGGA
CCCCAAAGAGCTTTCATTGTATCTATTGATTTTTACCACATTAGCAATTA¹AACTGAGAAAT
GGGCCGGGCACGGTGGCTCACGCCGTGAATCCAGCACTTTGGGAGGCCGAGGCGGGTGGAT
CACCTGAGATCAGGAGTTCAGACCAGCCTGGCCAACATGGTGAAACCTTGTCTACTAAAAA
TACAAAAAATTAGCCAGGCACAGTGGTGTGCACTGGTAGTCCAGTTACTCGGAGGCTGAG
GCAGGAAAAATCGCTTGAACCCAGGAGCGGACGTTGCGGTGAGCCGAGATCGCGCCGCTGAT
TCCAGCCTGGGCGACAAGAGTGAGACTCCATCTCACACA

MLPPALPPALVFTVAWSLLAERVSWSVRDAEDAHRLQPFVTERTLGKVQRWSGVHTQTGGRAG
GGQFCCAWLDSKRVLASPGWAANSIKNQRVWAPATESSAQLLCCWPVGVVARGGALCQ

FIGURE 285

GTCATGCCAGTGCCTGCTCTGTGCCTGCTCTGGGCCCTGGCAATGGTGACCCGGCCTGCCTCA
GCGGCCCCCATGGGCGGCCAGAAGTGGCACAGCATGAGGAGCTGACCTGCTCTTCCATGG
GACCTTGCAGCTGGGCCAGGCCCTCAACGGTGTGTACAGGACCACGGAGGGACGGCTGACAA
AGGCCAGGAACAGCCTGGGTCTCTATGGCCGCACAATAGAACTCCTGGGGCAGGAGGTCAGC
CGGGGCCGGGATGCAGCCAGGAACCTCGGGCAAGCCTGTTGGAGACTCAGATGGAGGAGGA
TATTCTGCAGCTGCAGGCAGAGGCCACAGCTGAGGTGCTGGGGGAGGTGGCCCAGGCACAGA
AGGTGCTACGGGACAGCGTGCAGCGGCTAGAAGTCCAGCTGAGGAGCGCCTGGCTGGGCCCT
GCCTACCGAGAATTTGAGGTCTTAAAGGCTCACGCTGACAAGCAGAGCCACATCCTATGGGC
CCTCACAGGCCACGTGCAGCGGCAGAGCGGGGAGATGGTGGCACAGCAGCATCGGCTGCGAC
AGATCCAGGAGAGACTCCACACAGCGGCGCTCCAGCCTGAATCTGCCTGGATGGAAGTGA
GACCAATCATGCTGCAAGGAACACTTCCACGCCCCGTGAGGCCCTGTGCAGGGAGGAGCTG
CCTGTTCACTGGGATCAGCCAGGGCGCCGGGCCCCACTTCTGAGCACAGAGCAGAGACAGAC
GCAGGCGGGGACAAAGGCAGAGGATGTAGCCCCATTGGGGAGGGGTGGAGGAAGGACATGTA
CCCTTTTCATGCCTACACACCCCTCATTAAGCAGAGTCGTGGCATTTCAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAA

FIGURE 286

MPVPALCLLWALAMVTRPASAAPMGGPELAQHEELTLFHGTLQLGQALNGVYRTTEGRLTK
ARNSLGLYGRTIELLGQEVSRGRDAAQELRASLLETQMEEDIILQLQAEATAEVLGEVAQAQK
VLRDSVQRLEVQLRSAWLGPAYREFEVLKAHADKQSHILWALTGHVQRQRREMVAQQHRLRQ
IQRHLHTAALPA

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FIGURE 287

GGCAACATGGCTCAGCAGGCTTGCCCCAGAGCCATGGCAAAGAATGGACTTGTAAATTTGCAT
 CCTGGTGTACCTTACTCTCTGGACCAGACCACCAGCCACACATCCAGATTAAAGCCAGGA
 AGCACAGCAAACGTCGAGTGAGAGACAAGGATGGAGATCTGAAGACTCAAATGAAAAAGCTC
 TGGACAGAAGTCAATGCCTTGAAGGAAATCAAGCCCTGCAGACAGTCTGTCTCCGAGGCAC
 TAAAGTTCACAAGAAATGCTACCTTGCTTCAGAAGGTTTGAAGCATTTCCATGAGGCCAATG
 AAGACTGCATTTCCAAAGGAGGAATCCTGGTTATCCCCAGGAACCTCCGACGAAATCAACGCC
 CTCCAAGACTATGGTAAAGGAGCCTGCCAGGTGTCAATGACTTTTGGCTGGGCATCAATGA
 CATGGTCACGGAAGGCAAGTTTGTGTACGTCAACGGAATCGCTATCTCCTTCCTCAACTGGG
 ACCGTGCACAGCCTAACGGTGGCAAGCGAGAAAACCTGTGTCTGTCTCCCAATCAGCTCAG
 GGCAAGTGGAGTGATGAGGCCTGTGCGAGCAGCAAGAGATACATATGCGAGTTTACCATCCC
 TAAATAGGCTCTTTCTCCAATGTGTCTCCAAGCAAGATTATCATATAACTTATAGGTTTCATGA
 TCTCTAAGATCAAGTAAAAATCATAATTTTACTTATTAAAAAATGCAACACAAGATCAAT
 GTCCATAGCAATATGATAGCATCAGCCAATTTTGCTAACACATTTCTTTGGGATTTTGGCCT
 TCCTGGGGTATAGGGGATCAGAAATATTGATCCATGTGCACGCAGATAAAATGGCTTCTGCT
 AAACAGACTAAAATCTTTCTCTAGTCTTTCTCACTTGTAACACCCAGTTTGTGTTTCAA
 AAATCACAGTAGCAATGCAACTCATCACTCTAGAAAAGCAAGCTTAGGCTACCTGAAAGATT
 TTCCCTTGGAAGTTTAGCGTATGTTTGACTAACAAAAATCCCTACATCAGAGACTCTAGGT
 GCTATATAATCCAAAAACTTTCAGCCTGTGTGCTCATTCTGTCCCATGCTGGCAATAATACC
 TTGTCAGCCCATTACCCTTATTTGAATTGCTCCATCTCCTGGTGGGACTTGTATCTGTGCT
 GCCATATCAGAACACAAACCCCTGAAGAGGTTCTGATTTGATTTTTTTTTTTTCTTCATGCC
 TACCCTTTTTTTGGAAGTTTCCAGCCGCAATTTGAAATGAAATGACAAGGTGTATATTGAT
 CAATTTTCATTCCCACCATTGCATTACAACCTCTAACTTAAATGGGTAAACCTAAGGCATAT
 CAAAGAAGCAGATTGCATGATAAACGGAAATAGAAAAAAGAACCTACATTTATTTTGCTTT
 AGCATCCTTACTCTACCTTTTATGAGATTGAGAGTGGACTTACATTTCCCTTTTACATTT
 TCGTATATTTATTTTTTTTAGCCATCATTATGTTTAAAGTCTATTATGGGAACCAATCTT
 TGGAAGCTGAAACCTGAATTTAAGAATGCTATCTTGGAAAATTGCATACGCTCTGTGCAATT
 TTTTATTCTGCCTAGTGCTATTCTGCTTGTTTAACTAGATTGTACAAAATAACTTCATTGCT
 TAATATCAAATTACAAAGTTTAGACTTGGAGGGAAATGGGCTTTTGAAGCAACCAATTT
 AAATATATTTTGTCTTCAAATAAATAGTGTTTAAACATTGAATGTGTTTGTGAACAATAT
 CCCACTTTGCAAACCTTAACTACACATGCTTGAATTAAGTTTTAGCTGTTTTTCATTGCTCA
 ATAATAAAGCCTGAATTCGATCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 288

MAQQACPRAMAKNGLVICILVITLLLDQTTSHTSRLKARKHSKRRVRDKDGLKTQIEKLWT
EVNALKEIQALQTVCLRGTKVHKCYLASEGLKHFHEANEDCISKGGILVIPRNSDEINALQ
DYGKRSLPGVNDFWLGINDMVTEGKFVDVNGIAISFLNWDRAQPNGGKRENCVLFSSQAQ GK
WSDEACRSSKRYICEFTIPK

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GCGAGGACC GGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGAGGTTCCCCGCGCGC
CCCCAGCCCCCGCGCCATGAAGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCCTGCA
GCTCCGCTGCTGCTTTCTTAGTGGGCTCGGCCAAGCCTGTGGCCACGCTGTCGTGCGCTG
GAGTCGGCGGGCGAGGCCGGGGCCGGGACCTGGCCAACCCCTCGGCACCTCAACCCGCT
GAAGCTCTGCTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCAGAAGT
GTGTGGCTGAGCTGGGTCCCCAGGCCGTGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGG
GCCCTGACAGTGTTTGGCTTGAGCCGAGACTGGAGCATCTACACCTGAGGACAAGACGCTGCC
CACC CGCAGGGGTGAAAACCCCGCGGGGAGGACGCTCCATCCCTTCCCCCGGCCCT
CTCAATAAACGTGGTTAAGAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAA

FIGURE 291

TGAAGGACTTTTCCAGGACCCAAAGGCCACACACTGGAAGTCTTGCAGCTGAAGGGAGGCACT
 CCTTGGCCTCCGCAGCCGATCACATGAAGGTGGTGCCAAGTCTCCTGCTCTCCGTCTCCTG
 GCACAGGTGTGGTGGTACCCGGCTTGGCCCCAGTCTCAGTCGCCAGAGACCCAGCCCC
 TCAGAACCAAGACCAGCAGGGTAGTGCAGGCTCCAGGGAGGAAGAGAGATGAGCAGGAGG
 CCAGCGAGGAGAAGCCGGTAGGAAGAGAAAGCCTGGCTGATGCCAGCAGGCAGCAGCTT
 GCCAAGGAGACTTCAAACCTCGGATTACGCCTGCTGCGAAAGATCTCCATGAGGCACGATGG
 CAACATGGTCTTCTCTCCATTGGCATGTCCTTGGCCATGACAGGCTTGATGCTGGGGGCCA
 CAGGGCCGACTGAAACCCAGATCAAGAGAGGGCTCCACTTGCAGGCCCTGAAGCCCAACAG
 CCCGGCTCTGCTTCCCTCTTTAAGGGACTCAGAGAGACCCTCTCCGCAACCTGGAAC
 GGGCCCTCTCACAGGGGAGTTTGCCTTCAATCCACAAGGATTTTGATGTCAAAGAGACTTTCT
 TCAATTTATCCAAGAGGTATTTTGATACAGAGTGCCTGATGAATTTTCGCAATGCCTCA
 CAGGCCAAAAGGCTCATGAATCATTACATTAACAAAAGAGACTCGGGGAAAAATCCCAAAC
 GTTTGATGAGATTAATCCTGAAACCAAATTAATTTCTGTGGATTACATCTTGTCAAAGGGA
 AATGGTTGACCCCATTTGACCTGTCTTACCAGAGTCGACACTTTCCACCTGGACAAGTAC
 AAGACCATTAAAGTGCCCATGATGTACGGTGCAGGCAAGTTGCTCCACCTTTGACAAGAA
 TTTTCGTTGTCATGTCCTCAAACCTGCCCTACCAAGGAAATGCCACCATGCTGGTGGTCTCA
 TGGAGAAAATGGGTGACCACCTCGCCCTTGAAGACTACCTGACCACAGACTTGGTGGAGACA
 TGGCTCAGAAACATGAAACCAGAAACATGGAAGTTTCTTTCCGAAGTTCAAGCTAGATCA
 GAAGTATGAGATGCATGAGCTGCTTAGGCAGATGGGAATCAGAAGAATCTTCCACCTTTG
 CTGACCTTAGTGAACCTCTCAGCTACTGGAAGAAATCTCCAAGTATCCAGGGTTTACGAAGA
 ACAGTGATTGAAGTTGATGAAGGGGCACTGAGGCAGTGGCAGGAATCTTGTGAGAAATTAC
 TGCTTATTCATGCTCCTGTCTATCAAAGTGGACCGGCCATTTCAATTCATGATCTATGAAG
 AAACCTCTGGAATGCTTCTGTTCTGGGCAGGGTGGTGAATCCGACTCTCCTATTAATTCAGG
 ACATGCATAAGCACTTCTGCTGTAGTAGATGCTGAATCTGAGGTATCAAACACACACAGGA
 TACCAGCAATGGATGGCAGGGGAGAGTGTCTTTTGTCTTAACTAGTTTAGGGTGTCTC
 AAATAAATACAGTAGTCCCCACTTATCTGAGGGGGATACATTCAAAGACCCCCAGCAGATGC
 CTGAAACGGTGGACAGTGTGAACCTTATATATATTTTCTTACATACATACCTATGAT
 AAAGTTTAAATTTATAAATTAGGCACAGTAAGAGATTAAACAATAAACAACATTAAGTAAAA
 TGAGTTACTTGAACGCAAGCACTGCAATACCATAACAGTCAAACCTGATTATAGAGAAGGCTA
 CTAAGTGACTCATGGGCGAGGAGCATAGACAGTGTGGAGCAATTGGCAGAGGGAGAAATTA
 CATCTGGGTGGACAGAGCAGGACGATGCAAGATTCCATCCCACTACTCAGAATGGCATGC
 TGCTTAAAGCTTTTAGATTGTTTATTTCTGGAATTTTTCATTTAATGTTTGGACCATGGT
 TGACCATGGTTAACTGAGACTGCAGAAAGCAAAACCATGGATAGGGGAGGACTACTACAAA
 GCATTAAATTGATACATATTTTTTAAAAAAAAAAAAAAAAAAAA

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FIGURE 292

MKVVP S L L L S V L L A Q V W L V P G L A P S P Q S P E T P A P Q N Q T S R V V Q A P R E E E E D E Q E A S E E K A G E
E E K A W L M A S R Q Q L A K E T S N F G F S L L R K I S M R H D G N M V F S P F G M S L A M T G L M L G A T G P T E T Q I
K R G L H L Q A L K P T K P G L L P S L F K G L R E T L S R N L E L G L S Q G S F A F I H K D F D V K E T F F N L S K R Y F
D T E C V P M N F R N A S Q A K R L M N H Y I N K E T R G K I P K L F D E I N P E T K L I L V D Y I L F K G K W L T P F D P
V F T E V D T F H L D K Y K T I K V P M M Y G A G K F A S T F D K N F R C H V L K L P Y Q G N A T M L V V L M E K M G D H L
A L E D Y L T T D L V E T W L R N M K T R N M E V F F P K F K L D Q K Y E M H E L L R Q M G I R R I F S P F A D L S E L S A
T G R N L Q V S R V L R R T V I E V D E R G T E A V A G I L S E I T A Y S M P P V I K V D R P F H F M I Y E E T S G M L L F
L G R V V N P T L L

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FIGURE 293

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCAGACATGAG
GAGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAG
CACCCAAGGTCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAG
GCCTGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGTCTTCCC
TGTCCAGAAGCCGAAACTCTTGACCACCGAGGAGAAGCCACGAGGTCAGGGCAGGGGCCCCA
TCCTTCCAGGCACCAAGGCCTGGATGGAGACCGAGGACACCTGGGCCGTGTCTGAGTCCC
GAGCCCGACCATGACAGCCTGTACCACCCTCCGCCTGAGGAGGACCAGGGCGAGGAGAGGCC
CCGGTTGTGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGAGGAAGACCAAGACCACA
TCTACCACCCCAAGTAGGGCTCCAGGGGCCATCACTGCCCCGCCCTGTCCCAGGCCAGG
CTGTGGGACTGGGACCCTCCCTACCCTGCCCCAGCTAGACAAATAAACCCAGCAGGCAAA
AAAAAAAAAAAAAAAA

FIGURE 294

MRLLLLVTSLVVVLLWEAGAVPAPKVPIKMQVKHWPSEQDPEKAWGARVVEPPEKDDQLVVL
FPVQKPCLLTTEEKPRGQGRGFILPGTKAWMETEDTLGRVLSPEPDHDSLYHPPPEEDQGEE
RPRLWVMPNHQVLLGPEEDQDHIYHPQ

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FIGURE 295

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTG
 TACCCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGC
 TGTTCCTCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAA
 TGGACCTGTTCTTCGTCTCCATCTCTGCCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCC
 TAGTGCAATTTGATGGCCTGTATTTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTTCT
 GTGACATGACCTCTGGGGGTGGCGGCTGGACCTGGTGGCCAGCGTGCATGAGAATGACATG
 CGTGGGAAGTGACGGTGGGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCC
 AGAGGGGGACGGCAACTGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCG
 ATGACTACAAGAACCCTGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCAGCTG
 CCCAATAAGTCCCCATGCAGCACTGGAGAAACAGCTCCCTGCTGAGGTACCGCACGGACAC
 TGGCTTCCTCCAGACACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCAGTGAAAT
 ATGGAGAAGGAAAGTGTGGACTGACAACGGCCCGGTGATCCCTGTGGTCTATGATTTTGGC
 GACGCCCAGAAAACAGCATCTTATTACTCACCTATGGCCAGCGGGAATTCAGTGCGGGATT
 TGTTCACTCAGGGTATTTAATAACGAGAGAGCAGCAACGCCTTGTGTGCTGGAATGAGGG
 TCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAGGATACTTCCAGAGGCCAGT
 CCCAGCAGTGTGGAGATTTTCTGGTTTTGATTGGAGTGGATATGGAACCTCATGTTGGTTA
 CAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCGTTGAGAGTTTGTG
 GGAGGGAACCCAGACCTCTCTCCCAACCATGAGATCCCAAGGATGGAGAACAACTTACCCA
 GTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAATCATATTGACTCAAGAAAAAAA

FIGURE 296

MNQLSFLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTEN
GVIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFG
SAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGLI
YQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYYSYPYGQREFTAGFVQFRVFNNERAAN
ALCAGMRVTGCNTEHHCIGGGGYFPEASPPQCGDFSGFDWSGYGTHVGYSSSREITEAAVLL
FYR

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FIGURE 297

CGCGAGGCCGGCGCCGGCTGCGCAGAGGAGCGCGTCTCGCCGCCGCCACCTCGGCTGGGAGCC
CACGAGGCTGCCGCATCTGCCCCGGAACA**ATGC**GGACTCGGCGCGCGAGGTGCTTGGGCCG
CGCTGCTCCTGGGGACGCTGCAGGTGCTAGCGCTGCTGGGGGCGCCCATGAAAGCGCAGCC
ATGGCGGCATCTGCAAACATAGAGAATTCTGGGCTTCCACACAACCTCCAGTGCTAACTCAAC
AGAGACTCTCCAACATGTGCTTCTGACCATACAAATGAACTTCCAACAGTACTGTGAAAC
CACCAACTTCAGTTGCCCTCAGACTCCAGTAATACAACGGTCACCACCATGAAACCTACAGCG
GCATCTAATACAACAACACCAGGGATGGTCTCAACAAATATGACTTCTACCACCTTAAAGTC
TACACCCAAAACAACAAGTGTTCACAGAACACATCTCAGATATCAACATCCACAATGACC
TAACCCACAATAGTTCAGTGACATCTGCTGCTTCATCAGTAACAATCACAACTATGCAT
TCTGAAGCAAAGAAAGGATCAAAATTGATACTGGGAGCTTTGTTGGTGGTATTGTATTAAC
GCTGGGAGTTTTATCTATTCTTTACATTGGATGCAAATGTATTACTCAAGAAGAGGCATT
GGTATCGAACCATAGATGAACATGATGCCATCATT**TAA**GGAATCCATGGACCAAGGATGGA
ATACAGATTGATGCTGCCCTATCAATTAATTTTGGTTTATTAATAGTTTAAACAATATCT
CTTTTGGAAATAGTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAAATATGTA
AAGATTCTTCAAGGTAACAAGGGTTTGGGTTTTGAAATAAACATCTGGATCTTATAGACCGT
TCATACAATGGTTTTAGCAAGTTCATAGTAAGACAAACAAGTCCTATCTTTTTTTTGGCT
GGGGTGGGGGCATTGGTCACATATGACCGATAATTGAAAGACGTCATCACTGAAAGACGAA
TGCCATCTGGGCATACAAATAAGAAGTTTGTACAGCATCAGATATTCTTTGGTATCTTTTGT
AGCTCACATAAAGAACTTCAGTGCTTTTCAGAGCTGGATATATCTTAATTACTAATGCCACA
CAGAAATTATACAATCAACTAGATCTGAAGCATAAATTTAAGAAAAACATCAACATTTTTTG
TGCTTTAACTGTAGTAGTTGGTCTAGAAACAAAATACTCC

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CAGCGCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGG
TCGCGGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCAGCG**ATG**CGCAGCCCTGTGGGGAGCG
CTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTGCTGCCGCGCTTTCGCTGCTGCTGCTGGC
GCAGCTGTCAGACGCCGCCAAGAATTTGAGGATGTCAGATGTAATGTATCTGCCTCCCT
ATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCTT
CATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAAGAAGCATACTGTCTACGCTGTGA
ATGCAAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTTATAATTTATCTCTCCA
TTTTGGGCCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGG
CGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCTTT
TGCAAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAAAGTGCTGAACAAGGTAG
AATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTGCTGCTTTGACCGG
CATGTTGTCTCAGC**TAA**TATGGGAATGTAATTCAAGTGATAGAAAGAAACAGGCAGACAA
CTTGGAAAGAACTGACTGGGTTTGCTGGGTTTCATTTTAAATCCTTGTGATTTTACCAACT
GTGTGCTGGAAGATTGGAAGCTGGAAGCAAAACTTGCTTGATTTTTTTTTCTTGTTAACGTA
ATAATAGAGACATTTTTAAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCTATTTG
TGACTTTTACTAATAAAAAATAAATCTGCCTGTAAATTATCTTGAAGTCCTTTACCTGGAACA
AGCACTCTCTTTTTACCACATAGTTTTAACTTGACTTTCAAGATAAATTTACGGGTTTTTG
TTGTTGTTGTTTTTTGTTTGTGTTGTTTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTT
AACAACCTTTTTTCAAGTCACTTTACTAAACAACTTTTGTAATAGACCTTACCTTCTATTG
TCGAGTTTCATTATATTTTGCAGTGTAGCCAGCCTCATCAAGAGCTGACTTACTCATTTG
ACTTTTGCACGTACTGTATTATCTGGGTATCTGCTGTGCTGCACTTCATGGTAAACGGGAT
CTAAAATGCCTGGTGGCTTTTCACAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATG
CAATGCATCCTAGAACAAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTG
GTGTGTGTGGTCTTACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACT
TGCAATAAAGAAATTTTATTTAAGCCCAAGCCTCCCTGGATTGATAATATACACATTTG
TCAGCATTTCCGGTCGTGTTGTAGAGCCAGCTGTTTGAGGTCCAATATGTGCAGCTTTGAAC
AGGGCTGGGGTTGGGGTGCCCTTCTCGAAGGTTCAACCATATTGGATAACTGGCTTTTT
TCTTCCATGTGCTCTCTTTGGAATGTAAACAATAAAAAATAATTTTTGAAACATCAA

FIGURE 301

GCACCTGCGACCACCGTGAGCAGTCATGGCGTACTCCACAGTGCAGAGAGTCGCTCTGGCTT
CTGGGCTTGTCCTGGCTCTGTCGCTGCTGCTGCCAAGGCCTTCCTGTCCCGCGGGAAGCGG
CAGGAGCCGCCGCCGACACCTGAAGGAAAATTGGGCCGATTTCCACCTATGATGCATCATCA
CCAGGCACCCCTCAGATGGCCAGACTCCTGGGGCTCGTTTCCAGAGGTCTCACCTTGCCGAGG
CATTTGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGGAAGAGGTCTG
ATGGGGCAGATTATTCCAATCTACGGTTTTTGGGATTTTTTTATATATACTGTACATTCTATT
TAAGGTAAGTAGAATCATCCTAATCATATTACATCAATTGAAAATCTAATATGGCGATAAAAA
TCATTGTCTACATTAAAACTTCTTATAGTTCATAAAATTATTTCAAATCCATCATCTCTTTA
AATCCTGCCTCCTCTTCATGAGGTACTTAGGATAGCCATTATTTCAAGTTTCACATAAGAATG
TTTACTCAATGTTTAAGTGTTTTGCCCCAAAATTCACAATAACAAGGCAGAACTAGGACTT
GAACATGGATCTTTTGGTTCTTAATCCAGTGAGTGATACAATTCAATGCACTCCCCTGCCA

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MAYSTVQRVALASGLVLALLSLLPKAFLSRGKRQEPPTPEGKLGFRPPMMHHHQAPSDGQT
 PGARFQRSHLAEAFKAKGSGGGAGGGSGRGLMGQIIPYGFGLYILYILFKVSRIILI
 ILHQ

MAYSTVQRVALASGLVLALLSLLPKAFLSRGKRQEPPTPEGKLGFRPPMMHHHQAPSDGQT
 PGARFQRSHLAEAFKAKGSGGGAGGGSGRGLMGQIIPYGFGLYILYILFKVSRIILI
 ILHQ

FIGURE 303

CGGCTCGAGTGCAGCTGTGGGGAGATTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATCTT
GGATTGAAAGTTGAGAGCAGCATGTTTTGCCCACTGAAACTCATCTCTGCTGCCAGTGTTAC
TGGATTATTCCTTGGGCCTGAATGACTTGAATGTTTCCCGCCTGAGCTAACAGTCCATGTG
GGTGATTTCAGCTCTGATGGGATGTGTTTTCCAGAGCACAGAAGACAAATGTATATTCAAGAT
AGACTGGACTCTGTCAACCAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTACTCCA
ATCTCAGTGTGCCTATTGGGCGCTTCCAGAACC GCGTACACTTGATGGGGACATCTTATGC
AATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGA
AATCCGCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTACTGCATGTGCTTCCAG
AGGAGCCCAAAGAGCTCATGGTCCATGTGGGTGGATTGATTGAGATGGGATGTGTTTTCCAG
AGCACAGAAGTGAACACGTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCGCAAAGGA
GGAGATTGTATTTCTGTTACTACCACAACTCAGGATGTCTGTGGAGTACTCCAGAGCTGGG
GCCACTTCCAGAAATCGTGTGAACCTGGTGGGGACATTTTCCGCAATGACGGTTCATCATG
CTTCAAGGAGTGAGGGAGTCAGATGGAGGAACTACACCTGCAGTATCCACCTAGGGAACCT
GGTGTTCAGAAAACCATTTGTGCTGCATGTCAGCCCGGAAGACCTCGAACACTGGTGACCC
CGGCAGCCCTGAGGCCTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTGTGGGAATTGTC
TGTGCCACAATCCTGCTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGAAATAA
GAGTTCAGTGAATTCTACAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAAG
AAAAACCCCTGCCATTTTGAAAGATGTGAAGGGGAGAAACACATTTACTCCCAATAATTGTA
CGGGAGGTGATCGAGGAAGAAGAACCAAGTGA AAAATCAGAGGCCACCTACATGACCATGCA
CCAGTTTGCCCTTCTCTGAGGTCAGATCGGAACAACTCACTGAAAAAAGTCAGGTGGGG
GAATGCCAAAAACACAGCAAGCCTTTTGAAGAAGATGGAGAGTCCCTTCATCTCAGCAGCGG
TGAGAGCTCTCTCCTGTGTGTGTCCTGGGCCACTCTACCAGTGATTTGAGACTCCCGCTCTC
CCAGCTGTCTCCTGTCTCATTGTTTGGTCAATACACTGAAGATGGAGAATTGGAGCCTGG
CAGAGAGACTGGACAGCTCTGGAGGAACAGGCCCTGCTGAGGGGAGGGGAGCATGGACTTGGC
CTCTGGAGTGGGACACTGGCCCTGGGAACAGGCTGAGCTGAGTGGCCTCAAACCCCCGTT
GGATCAGACCCTCCTGTGGGCAGGGTCTTAGTGAGTGAATTAAGTGGGAAGAATCAGAGATA
AAAACCAACCCAAATCAA

FIGURE 304

MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLSPG
EHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDI LCNDGSLLLQDVQEADQGTYYICEIRLKGES
QVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHKVTKVEWIFSGRRAKEEIVFRYY
HKLMSVEYSQSWGHFQNRVNLVGDI FRNDGSIMLQGVRES DGGNYTCSIHLGNLVFKKTIV
LHVSPEEPRTLVT PAALRPLVLGGNQLV IIVGIVCATILLLPVLILIVKKTCGNKSSVNSTV
LVKNTKKTNP EIKEKPCHFERCEGEKHIYSP IIVREVIEEEEPSEKSEATYMTMHPVWPSLR
SDRNSLEKKSGGMPKTQQAF

FIGURE 305

CTATGAAGAAGCTTCTCTGAAAAACAATAAGCAAAGGAAAAACAAATGTGTCCCATCTCACATG
 GTTCTACCCCTACTAAAGACAGGAAGATCATAACTGACAGATACTGAAATTGTAAGAGTTGG
 AAACTACATTTTGCAAAGTCATTGAACTCTGAGCTCAGTTGCAGTACTCGGGAAGCCATGCA
 GGATGAAGATGGATACATCACCTTAAATATTAAGTAACTCGGAAACAGCTCTCGTCTCCGTG
 GCCCTGCATCCTCCTCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGG
 ATGGTTGTGGGCTGGTGGCTCTGGGGATTTGGTCTGTCATGCAGCGCAATTACCTACAAGA
 TGAGAATGAAAAATCGCACAGGAAGCTCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGG
 TAAAAAATCAGAACTAAAGGGCACTTTCAAAGGTCATAAATGCAGCCCCTGTGACACAAAC
 TGGAGATATTATGGAGATAGCTGCTATGGGTTCTTCAGGCACAACCTAACATGGGAAGAGAG
 TAAGCAGTACTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGG
 AGTACATCAAAGCCAGGACTCATTTAATTCGTTGGGTCGGATTATCTCGCCAGAAGTCGAAT
 GAGGTCTGGAAGTGGGAGGATGGCTCGGTTATCTCAGAAAAATATGTTTGAGTTTTTGAAGA
 TGGAAAAGGAAATATGAATTGTGCTTATTTTCATAATGGGAAAAATGCACCTACCTTCTGTG
 AGAACAAACATTATTAAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCT
TAATGCAAAGAGGTGGACAGGATAACACAGATAAGGGCTTTATTGTACAATAAAGATATGT
 ATGAATGCATCAGTAGCTGAAAAAAAAAAAAA

FIGURE 306

MQDEDGYITLNIKTRKPALVSVGPASSSWWRVMALILLILCVGMVVGLVALGIWSVMQRNYL
QDENENRTGTLQQLAKRFCQYVVKQSELKGTGFKGHKCSPCDTNWRYYGDSCYGFRRHNLWE
ESKQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGLSRQKSNEVVKWEDGSVISENMFEFL
EDGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQLP

FOUO" 1140660

FIGURE 307

CCCACGCGTCCGCGCAGTCGCGCAGTTCTGCCTCCGCTGCCAGTCTCGCCCGCATCCCGG
 CCCGGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCGCGCGGGAGCCGGACCGC
 CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCGAGTGGGAGAA
 GCCCCGGCAAACGCAAGCTAAGGAGACCAAAGCGGCAGAGTCGCGAGACAGCGGACAAGCAG
 CGGAGGAGAAGGAGGAGGAGGCGAACCAGAGAGGGGCAGCAAAGAAGCGGTGGTGGTGGG
 CGTCGTGGCC**CATG**GCGGCGGCTATCGCCAGCTCGCTCATCCGTGAGAAGAGGCAAGCCCGCG
 AGCGCGAGAAATCCAACGCCTGCAAGTGTGTGAGCAGCCCCAGCAAAGGCAAGACCAGCTGC
 GACAAAAACAAGTTAAATGTCTTTCCCGGGTCAAACCTCTTCGGCTCCAAGAAGAGGCGCAG
 AAGAAGACCAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACC
 ACTTGCAGCTGCAGGCGGATGGAACCATTGATGGCACCAAAGATGAGGACAGCACTTACACT
 CTGTTTAAACCTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT
 GTACTTGGCAATGAACAGTGAGGGTACTTGTACACCTCGGAACCTTTTACACCTGAGTGCA
 AATTCAAAGAATCAGTGTGTGAAAAATTATTATGTGACATATTCATCAATGATATACCGTCAG
 CAGCAGTCAGGCCGAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA
 CCATGTGAAGAAGAACAAAGCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGGCCATGT
 ACAAGGAGCCATCACTGCAGGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACC
 AAGAGCAGAAGTGTCTCTGGCGTGCTGAACGGAGGCATAATCCATGAGCCACAATGAATCAAC
GTAGCCAGTGAGGGCAAAGAAGGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAAT
 TCTTCTAGCAGTCCTTCACCCAAAAGTTCAAATTTGTCAGTGACATTTACCAAACAAACAGG
 CAGAGTTCACATATTCTATCTGCCATTAGACCTTCTTATCATCCATACTAAAGC

FIGURE 308

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498

><subunit 1 of 1, 245 aa, 1 stop

><MW: 27564, pI: 10.18, NX(S/T): 1

MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGKTSCKDNKLNVSFVKLFSGSKKRRRRP
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTDKEDSTYTLFNLIPVGLRVVAIQGVQTKLYLA
MNSEGILYTSELFTECKFKESVFENYYVTYSSMIYRQQSGRGWYLGLENKEGEIMKGNHVK
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKSRSVSGVLNGGKSMHNEST

N-glycosylation site.

amino acids 242-246

Glycosaminoglycan attachment site.

amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site.

amino acids 93-100

N-myristoylation site.

amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop).

amino acids 231-239

HBGF/FGF family proteins

amino acids 78-94, 102-153

FIGURE 309

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGGG
 ACTTGTTGTAAGAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTTACTGAACCTGGG
 CAACCTGGATATTCTGAGACATATTTTGGGGGGATTTCAGTGAAAAAAGTGGGGGATCCCCCT
 CCATTTAGAGTGTAGCAAAGGAAAAAACACCAAGGTTGGGTTCCCTCCTGACATTGGCAGTG
 CCCCAGTAGGGTGGGATGAGCGAATATTCCCAAAGCTAAAGTCCACACCCCTGTAGATTAC
 AAGAGTGGATTGTCAGGAGTGTGCCCCAAAATACAGTGGAAAGTGCTGAAGATATTTAA
 ACCACGTCCTTGAAAATTTAGTGGGCTTGGCTTTGGGATAGGTGAAGTGAGGACAGACACTG
 GAGAGGAGGGAAAGGGACGTTTTCAATAGGAGGCAAAACCTCAGGGTGGGATCCACTGAGG
 AGTACATAGGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCACGGGTGGTAAGTGGCTGCT
 GTGGAGGGGGTACGTGAGGGGGGGGTCTGGGGCTTATCCTCAGGTCTGTGGGTGGGGCAG
 CGAGTCGGGGCCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGGAGCCAG
 CGCGCTCCGGGGCCTGCCGGTTTGGGGGTGTCTCCTCCCGGGGCCTATGCGCGGCGCTGGC
 CAGTAGCCTGATCCGGCAGAAGCGGGAGGTCCGCGAGCCCGGGGCGAGCCGGCCGGTGTGCGG
 CGCAGCGGCGCTGTGTCCCCGCGGCACCAAGTCCCTTTGCCAGAAGCAGCTCCTCATCCTG
 CTGTCCAAGGTGCGACTGTGCGGGGGGGCGGCCCGCGCGGCGGACCGCGGCCCGGAGCCTCA
 GCTCAAAGGCATCGTCACCAAACTGTTCTGCCGCCAGGGTTTCTACCTCCAGGCGAATCCCG
 ACGGAAGCATCCAGGGCACCCAGAGGATACCAGCTCCTTCACCCACTTCAACCTGATCCCT
 GTGGGCCTCCGTGTGGTCAACATCCAGAGCGCCAAGCTGGGTCACTACATGGCCATGAATGC
 TGAGGGACTGCTCTACAGTTTCGCCGATTTCACAGCTGAGTGTGCTTTAAGGAGTGTGTCT
 TTGAGAATTACTACGTCTGTACGCCTCTGCTCTCTACCGCAGCGTCGTTCTGGCCGGGCC
 TGGTACCTCGGCCTGGACAAGGAGGGCCAGGTCACTGAAGGGAACCGAGTTAAGAAGACAA
 GGAGCTGCCCACTTTCTGCCCAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCC
 ACAGTGTCCCCGAGGCCTCCCTTCCAGTCCCCCTGCCCCCTGAAGTGTAGTCCCTGGACTG
 GAGGTTCCCTGCACTCCAGTGAGCCAGCCACCACCACAACCTGT

FIGURE 310

MAALASSLIRQKREVREPGGSRPVSAQRRVCPRGKSLCQKQLLILLSKVRLCGGRPARPDR
GPEPQLKGIVTKLFCRQGFYLANPDGSIQGTPEDTSSFTHEFNLI PVGLRVVTIQSAKLGHY
MAMNAEGLLYSSPHFTAECRFKECVFENYVLYASALYRQRRSGRAWYLGLDKEGQVMKGNR
VKKTKAAAHFLPKLLEVAMYQEPSLHSVPEASPPSPAP

Tyrosine kinase phosphorylation site:

amino acids 199-207

N-myristoylation sites:

amino acids 54-60, 89-95, 131-137

HBGF/FGF family signature:

amino acids 131-155

FIGURE 311

ATGGCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGCGGGAGCAGCACTG
GGACCGGCCCTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACC GCGGGCTCTGCAACG
GCAACCTGGTGGATATCTTCTCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG
CGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTT
GCAAATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCT
TCAACCTCATACCAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAAAGGGTTGTAT
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTT
TAAAGAATCTGTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG
AATCTGGTAGAGCCTGGTTTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGA
GTAAAGAAAACCAAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCG
AGAACCATCTTTGCATGATGTTGGGGAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAA
GCACAAGTGCCTCTGCAATAATGAATGGAGGCAAACCAGTCAACAAGAGTAAGACAACATAG

FIGURE 312

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503

><subunit 1 of 1, 247 aa, 1 stop

><MW: 27702, pI: 10.36, NX(S/T): 2

MAAAIASGLIRQKRQAREQHWDPRPSASRRSSPSKNRGLCNGNLVDIFSKVRIFGLKKRRLR
RQDPQLKGIVTRLYCRQGYLQMHPDGDGTDKDDSTNSTLFLNLIQVGLRVVAIQGVKTGLY
IAMNGEGYLYPSELFTECKFKESVFENYVYIYSSMLYRQQESGRAWFLGLNKEGQAMKGNR
VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKSSTT

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins.

amino acids 104-155, 171-198

GGGGAGGAGGAATTGACCAITGAAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTGGGTGCCTTGCAAAAAT
GARGGATGCAGGAGCGAGCTTTCTCTCTGGAAACCGAACGCAATGGATAAATCATGATTGTGCAGAGAGAGGAGGA
ACGAAGCTTTTCTTGTGAGCCCTGGATCTTAAACGCAAAATGTGTATATGTGCACACAGGGAGCATTCAAGAT
AAATAAAACAGAGTTAGAACCCGCGGGGTTGGTGTGTTCTGACATAAATAAAATCTTAAAGCAGCTGTCC
CTCCCAACCCCCAAAAAAGAGAGGATGGTAAGAAAGAACCCAGGATTCAAAAGAAAAAGTATGTTCAATT
TTCTCTATAAAGGAGAAAAGTAGACCAAGGAGATATTTTTGGAATGAAAAGTTTGGGGCTTTTTAGTAAAGTAA
AGAACTGTGTGGTGGTGTGTTTCTCTTCTTTTGAATTGCCACAGAGGAGAGGAAATTAATAATACATCTGC
AAGAAATTTAGAGAGAAGAAAAGTTGACCGCGGCAGATTGAGGCATTGATTGGGGAGAGAAAACCGACGAGCA
CAGTTTGATTTTCTGATATGTTGACATAAAATGACGGATAATTGCAGTTGGATTTTCTTCATCAACCTCTTT
TTTTTAAATTTTTATCCTTTTTGGTATCAAGATCATGCGTTTTTCTCTGTCTTAACCACTGATTTCATCT
GGATGTTGCTGTGATCAGTCTGAAATACAACCTGTTGAATTCAGAAGGACCAACACCGAGATAAATATGAATG
TTGAACAAGATGACCTTACATCCACAGCAGATAATGATAGGTCTAGGTTTACAGGGGCCCTATTGACCCCT
GCTTGTGTGTCTGCTGCTGGCTCTTCAACTCTTGTGTGGTGGTGGTGTGTGTGGCGGCTCAGACCTGCCCTTCTGTGT
GCTCTGCGACCAACCGATTGACGAAGGTGATTTGTGTCGAAAAACCTCGCTGAGGTTCCGGATGGCATCTCC
ACCAACAGACCGGTGCTGAACTCCATGAGAACCAATCCAGATCAAAAGTGAAACGCTTCAAGCACTTGAG
GCACCTTGGAAATCCTATGCTTGTAGTAGGAACCATACAGAACCATTGAAATGGGGCTTCAATGGTCTGGCGA
ACCTCAACACTCTGGAACCTTTGACAATCGTCTTACTACCATCCGAATGGAGCTTTTGTATACTTGTCTAAA
CTGAAGGAGCTCTGGTTGCGAAACAACCCCAATTGAAAGCATCCCTTCTTATGCTTTTAAACAGAATTCTCTCTTT
GCGCGACTAGACTTAGGGGAATTGAAAAGACTTTATACATCTCAGAAGTGCCCTTTGAAGCTTGCTTCCCACT
TGAGGATTTTGAACCTTGCCATGTGCAATGCGGTAATCCGGAACCTCACACCGCTCATAAACATAGATGAG
CTGGATCTTTTGGGAATCATTTATCTGCCATCAGGCCTGGCTCTTTCCAGGGTTTGATGCACCTTCAAAACT
GTGGATGATACAGTCCAGATTCAAGTGATTGAACGGAATGCTTTGACAACTTCAGTCACTAGTGGAGATCA
ACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTCTTCACTCCCTTGATCACTCTAGAGCGGATACAT
TTACATCAACAACCTTTGGAAGTGAATCTGACATCTGTGGCTGAGTGGTGGATAAAGACATGCCCCCTC
GAACACAGCTGTGTTGCGCGGTGTAACACTCTGCCAATCTAAGGGGAGATTAACCTGGAGAGCTGCACGAGA
ATTACTTTCATGTCTATGTGCGCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCAGTGAAGGCATGGCAGCT
GAGCTGAATGTGCGGCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAAATGGAACAGTCTATGACACA
TGGGGCGTACAAAGTGCGGATAGCTGTGCTCAGTGATGTTACGTTAAATTTCAACCTGTAACCTGCAAGATA
CAGGACTGTACACATGTATGGTAGTAATCCGTTGGGAATCTACTGCTTCAGGACCCCTGAATGTTACTGCA
GCAACCACTACTCTCTTTCTTACTTTTCAACCGTGCAGCTAGAGACATGGAAACGCTCTCAGATGAGGACG
GACCACAGATAACAATGTGGGTCCCCTCCAGTGGTGCAGCTGGGAGACCCCAATGTACCACCTCTCTCACAC
CACAGAGCACAGGTTCGACAGAGAAAACCTTCAACATCCCAAGTACTGATATAAAGAGTGGGATCCAGGAATT
GATGAGGTCTATGAAGACTACCAAAATCATCATTGGGTGTTTTGTGGCCATCACACTCATGCTGAGTGTGCT
GGTCATTTTCTACAAGATGAGGAAGCAGCACCATCGGCAAAACCTACGCCCCAACAGGCTGTTGAAATTA
TTAATGTGATGATGAGATTACGGGAGACACACCGTAGGAAGCACTGCCATCGCCATGCGCTGTATCGAGCATGAG
CACCTAAATCACTATAACTCATACAATCTCCCTTCAACCACACAACACAGTTAACACAATAAATTCATACA
CAGTTCACTGATGACCGTTATTGATCCGAATGAACCTTAAAGACAATGTACAAGAGACTCAATCTAAAGACA
TTTACAGAGTTTCAAAAAAACAACCAATCAAAAAAAGAGACAGTTTATTAATAATGACACAAATGACTGGGCTAA
ATCTACTGTTTCAAAAAGGTCTTTTACAAAAAACA AAAAAGAAAAGAAATTTATTTATTAATAAATCTTATGT
TGATCTAAGACAGAAATAA

FIGURE 314

MLNKMTLHPQQIMIGPRFNALFDPLLVLALLQLLVVAGLVRAQTCPSVCSNQSFKVIC
 VRKNLREVPDGIISTNTRLNLHENQIQIIVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
 NLTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRDLGELKRLS
 YISEGAFEGLSNRLYNLAMCNLREIPNLTPLIKLDLDELDSGNHLSAIRPGSFQGLMHLQKL
 WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLHNPWNCNDIL
 WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
 LKCRASLTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVDGTGMYTCMVSNSVGN
 TTASATLNVTAATTPFSYFSTVTVETMEPSQDEARTDNNVGPTPVVDWETTNVTTSLTPQ
 STRSTEKTTFTIPVTDINSGIPGIDEVMKTKIIIGCFVAITLMAAVMLVIFYKMRKQHRQN
 HHAPTRTVEIINVDDITGDTPMESHLMPAIEHEHLNHYSYKSPFNHTTTVNTINSIHSS
 VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419,
 434-438, 442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
 391-397, 422-428, 433-439, 531-537

GC GCGCGGGAGCCCATCTGCCCCAGGGGCACGGGGCGCGGGGCGCGGTCCCGCCCGGCACAT
GGCTGCAGCCACCTCCGGCGCACCCGAGGGCGCCCGCCAGCTGCGCCCGAGGTCCTCGCGGA
GGCGCCGGCGCCGCCGAGCAACGACGAACATGAGCGGGGAAGCGCCGCTCGGGGATC
GGGATGTCCTCCTCCTTCTCCTCTTGCTAGTTTCTCATATATGTGGAACCTTGGGGATCA
CCTCAGATGATCAAGAGATGGCAGAGGAAAAGGCTTTGCCCTGCCACCTCAACTGGGGC
TTCCAGAAAAGAGACACTCTGGATATGTAATGGCTGCTCACCAGATAATGAAGGAAACAAAAA
GTGGTGATCACTTACTCTAGCTCGTCATGTCTACAATACTTGACTGAGGACAGAGAAGGCCG
AGTGGCCTTTGCTTCCAATTCTCGGCAGGAGATGCCCTCTGCAGATGAACTCTTGAA
CCAGTGATGAGGGCCGGTACACCTGTAAAGTTAAGAATTCAGGGCGCTACGTGTGGAGCCA
GTCACTTTAAAAGTCTTAGTGCAGACCATCAAGCCCAAGTGTAGTTTGAAGGAGAGCTGAC
AGAGAAGGATGACCTGACTGTTCGAGTGTGAGTCACTCTCGCACAGAGCCCATTTGTGTATT
ACTGGCAGCGAATCCGAGAGAAAAGAGAGAGATGAACCTCTGCCTCCCAAATCTAGGATT
GACTACAACCCACCTGGACGAGTCTGCTGAGGAATTTACCATTGCTCTACTCTGGACTGTA
CCAGTGCACAGCAGGCAACGAAAGCTGGGAAGGAAAGCTGTGTGGTGCGAGTAACGTGACAGT
ATGTACAAGACATCGGCATGGTTGCGAGGACGAGTGCAGGCCATAGTGAGCTGGAGCCCTGCTG
ATTTTCTCTTTGGTGTGGCTGTAATCCGAAGGAAGAACAAGAAAGGATGAGGAAGAAGA
GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAAGCCCGTCTTGTGAACCCAGCT
CCTCTTCTCAGGCTCTCGGAGCTCAGCTCTGTGTTCTTCTCCACTCTGCCTCCACAGCAAT
AGTGCTCTAGCGACGCGACGACCTGTCAACTGACGACGACCCACAGCGAGGCTGGCCAC
CCAGGCATACAGCTGTGTGGGCGCAGAGGTGAGAGGTTCTGAAACCAAGAAAGTCCACCAT
CTAATCTGCACCAAGCAGAAACCAAGCCAGCATGATCCCGACGACGAGAGCTTCCAA
ACGGTCTGTAATTAACATGGACTGACTCCACGCTTTCTTAGGAGTCAGGGTCTTTGGACTC
TTCTCGTCAATTGGAGCTCAAGTGCACAGCCACAACACAGATGAGAGGTCATTAAGTAGTA
CTGAGCATCTGACCGGAACGATTTCAGATGACATTTTCCCTATACAATACCAACAGCAAA
AGGATGTAAGCTGATTTCATCTGTAAAAGGCATCTTATTGTGCTTTAGACCAGAGTAGAGGG
AAAGCAGGAGTCCCAATCTATTTTGTACACAGGACCTGTGGTGAGAAGGTTGGGGAAGGGT
AGGTGAATATACCTAAAACCTTTAATGTGGGATATTTGTATCATGCTCTTGATTACAAAT
TTCAAGAGGAAATGGGATGCTGTTGTAAATTTTTCATGCAATTTCTGCAACTTATGGATT
ATTAGTTATTTCAGACAGTCAAGCAGAACCCACAGCCTTATACACCTCTACACCATGTAC
TGAGCTTAACCATCTTAAGAAACTCCAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAC
TTCATTTGTCTATAAGGTTTGGATATTAATTTCAAGGGAGTTGAAATAGTGGGAGGTGGAGA
AGAGTGAATGAGTTTCTCCACTCTATACCTAATCTCAATTTTGTATTGAGCCCAAAATAC
TATGAAAGGAGACAAAAATTTGTGACAAGGATGTGGAAGACCTTCTCATCTCTATGATGTT
ATGAGGATTTGTGACAAACATTAGAATATATATGGAAGCAATTTGGATTTCCCTCAAT
CAGATGCCCTCAAGGACTTTCTGCTAGATATTTCTGGAAAGGAGAAAAATACAACATGTCAAT
TATCAACGTCCTTAGAAGAAATTTCTCTAGAGAAAAGGAGATAGGAATGCTGAAGATTA
CCCAACATACCATTTATAGTCTCTCTTCTTGAGAAAAATGTGAACAGGAATGTGAACAGTGG
GTGGACTAGAAAGGGAGATTAGATCAGTTTTCTCTTAATATGCTCAAGGAAGGTAGCCGGCA
TGGTGCAGGCACCTGTAGGAAATCCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCC
ATTGCACTCAGCCTGGGTGCACAGAGCGGACTCGTCTC

FIGURE 316

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLLVSYVGTGLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTTEEQGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWVSHV
ILKVLVRPSKPKCELEGELETEGSDTLQCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLMTSYSGLYQCTAGNEAGKESCVVRVTVQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPPSSSSSGSRSSRSRSSSTRSTANS
ASRSQRTLSTDAAPQPLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

Over the Top

Over the Top

FIGURE 318

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA82361

><subunit 1 of 1, 352 aa, 1 stop

><MW: 38938, pI: 7.86, NX(S/T): 3

MALLLCFVLLCGVDFARSLSITTPPEEMIEKAKGETAYLPCKFTLSPEDQGGLDIEWLISPA
DNQKVDQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQCKVKK
APGVANKKIHLVVLVKPSGARCYVDGSEEIGSDFKIKCEPKESLPLQYEWQKLSDSQKMPT
SWLAEMTSSVISVKNASSEYSGTYSCTVRNRVGSDDQCLRLNVVPPSNKAGLIAGAIIGTLL
ALALIGLIIFCCRKKRREEKYKEVHHDIREDVPPPKSRTSTARSYIGSNHSSLGSMSPSNM
EGYSKTQYNQVPSEDFERTPQSPTLPPAKFKYPYKTDGITVV

Signal sequence.

amino acids 1-19

Transmembrane domain:

amino acids 236-257

N-glycosylation sites.

amino acids 106-110, 201-205, 298-302

Tyrosine kinase phosphorylation sites.

amino acids 31-39, 78-85, 262-270

N-myristoylation sites.

amino acids 116-122, 208-214, 219-225, 237-243, 241-247,
245-251, 296-302

Myelin P0 protein.

amino acids 96-125

FIGURE 319

TGAAATGACTTCCACGGCTGGGACGGAACTTCCACCCACAGCTATGCCTCTGATTGGTGA
 ATGGTGAAGTGCCGTGTCTAACTTTTCTGTAAAAAGAACCCAGCTGCCTCCAGGCAGCCAGCC
 CTC AAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTCGC
 CAATTTAACACCAAGAAGAATTGAGGCTGCTTGGGAGGAAGGCCAGGAGGAACACGAGACTG
 AGAGATGAATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCCCTTCTGCCCTC
 CTTTGTCTGGCGACAGCCTCTCAAATGCAGATGGTTGTGCTCCCTTGCCCTGGGTTTTACCTG
 CTTCTCTGGAGCCAGGTATCAGGGGCCAGGGCCAAGAATTCACCTTTGGGCCCTGCCAAGT
 GAAGGGGGTTGTTCCCCAGAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAG
 CTCAGGATAACATCACGAGTGCCCGGCTGCTGCAGCAGGAGGTTCTGCAGAACGTCTCGGAT
 GCTGAGAGCTGTTACCTTGTCCACACCCTGCTGGAGTTCTACTTGAAAACCTGTTTTCAAAAA
 CCACCACAATAGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCCAACAACAT
 TTGTTCTCATCGTGTACAAC TGCAACCCAGTCAAGAAAAAGAGATGTTTTCCATCAGAGAC
 AGTGCACACAGGCGGTTTTCTGTATTCCGGAGAGCATTCAACACAGTTGGACGTAGAAGCAGC
 TCTGACCAAAGCCCTTGGGGAAGTGACATTCTTCTGACCTGGATGCAGAAATCTACAAGC
 TCTGAATGTCTAGACCAGGACCTCCCTCCCCCTGGCACTGGTTTGTTCCTGTGTCATTTCA
 AACAGTCTCCCTTCCATGCTGTTCACTGGACACTTCACGCCCTTGCCATGGGTCCCATTTC
 TTGGCCAGGATTATGTCAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAG
 GTGCCTCTGGATGCTGTGAAGAGTCTACAGAGAAGATTCTTGATTTATTACAACCTATTTT
 AATTAATGTCAGTATTTCAACTGAAGTTCTATTTATTTGTGAGACTGTAAGTTACATGAAGG
 CAGCAGAATATTGTGCCCCATGCTTCTTTACCCCTCACAATCCTTGCCACAGTGTGGGGCAG
 TGATGGGTGCTTAGTAAGTACTTAATAAACTGTGGTGCTTTTTTTGGCCTGTCTTTGGATT
 GTTAAAAAACAGAGGGGATGCTTGATGTAAAACCTGAACCTCAGAGCATGAAAATCACACT
 GTCTTCTGATATCTGCAGGGACAGAGCATTGGGGTGGGGTAAGGTGCATCTGTTTGAAGG
 TAAACGATAAAATGTGGATTAAAGTGCCAGCACAAAGCAGATCCTCAATAAACATTTTCATT
 TCCCACCCACTCGCCAGCTCACCCCATCATCCCTTTCCCTTGGTGCCCTCCCTTTTTTTT
 TATCCTAGTCATTCTTCCCTAATCTTCCACTTGAGTGTCAAGCTGACCTTGCTGATGGTGAC
 ATTGCACCTGGATGTACTATCCAATCTGTGATGACATTCCCTGCTAATAAAAGACAACATAA
 CTC CAAAAA AAAAAAAAAAAAAAAAAAAAAA

FIGURE 320

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002
```

```
><subunit 1 of 1, 206 aa, 1 stop
```

><MW: 23799, pI: 9.12, NX(S/T): 3

MNFQQRQLSLWTLARFPCPLLATASQMOMVLPCLGFTLLLSQVSGAQGEFHGPCQVK
 GVPVQKLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSDAESCYLVTLLLEFYLKTVFNH
 HNRTVEVRTLKSFSTLANNFVLIVSQLQPSQENEMFSIRDSAHRRFLLFRRAFKQLDVEAL
 TKALGEVDILLTWMOKFYKL

Signal sequence:

amino acids 1-42

N-glycosylation sites.

amino acids 85-89, 99-103, 126-130

FIGURE 321

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGCATGAAGTTACAGTGTGTTCCCTTTGGCTC
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTCC
CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAGAGCCATCCAAGCTAAGG
ACACCTTCCCAAATGTCACTATCCTGTCCACATTGGGAGACTCTGCAGATCATTAAGCCCTTA
GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTCTACGTGGACAGGGTGTTCAAGGATCA
TCAGGAGCCAAACCCCAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTTCCTCTACA
TGCAGAAAACTCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC
AATGCCACCAGAGTCATCCATGACAACCTATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
ATCCCTGGGAGAGCTCGACGTCTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT
CAGCTTGATGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCTGTGCGGTTTACT
GTGGGAGACAGCCACCTTGAAGGGGAAGGAGATGGGGAAGGCCCTTGACAGTGAAAGTCC
CACTGGCTGGCCTCAGGCTGTCTTATCCGCTTGAAAATAGGCAAAAAGTCTACTGTGGTAT
TTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCTGGGAGTAAAGGGCTGCCTT
CCCATCTAATTTATGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT
GTAGTACACATTGTACTGAGTGGTTTTCTGAATAAATCCATATTTACCTATGA

FIGURE 322

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282
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```
><subunit 1 of 1, 177 aa, 1 stop
```

><MW: 20452, pI: 8.00, NX(S/T): 2

MKLQCVSLWLGLTILILCSVDNHGLRRLCLISTDMHHIEESFQEIKRAIQAKDTFPNVITILST
 LETLQIKPLDVCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ
 ROCHCRQEATNATRVIHNDYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

Signal sequence:

amino acids 1-18

N-glycosylation sites.

amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation site.

amino acids 24-30

Actinin-type actin-binding domain signature 1.

amino acids 159-169

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCACTTGGCTTCGTTAG
AACGCGGCTACAATTAATACATAACCTTATGTATCATACACATACGATTTAGGTGACACTAT
AGAATAACATCCACTTTTGCTTTCTCTCCACAGGTGCCACTCCAGGTCCAACCTGCACCTC
GGTTCTATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGCAGCATGTTGGGGGCCGCT
CAGGCTCTGGGTCTGTGCTTGTGCAGCGTCTGCAGCATGAGCGTCTCAGAGCCTATCCCA
ATGCTCCCCACTGCTCGGCTCCAGTGGGGTGGCTGATCCACCTGTACACAGGCCACAGCC
AGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCTATCAGAC
CATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGA
TGAGCAGAAGATACCTCTGCATGGATTTACAGAGCAACATTTTTGGATCACACTATTTTCGAC
CCGGAGAAGTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGCTTACCACTCTCC
TCAGTATCACTTCTGTGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCTGCGAGGCATGAACC
CACCCCCGTACTCCAGTTCTGTGCCGGAGGAACGAGATCCCCCTAATTCACCTTCAACACC
CCCATAACACGGCGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCCCTGAACGT
CTGAAGCCCCGGGCCGGATGACCCCGGCCCGGCTCTCTGTTACAGAGGACTCCCGAGCG
CGCAGGACAACAGCCCGATGGCCAGTGAACCATTAGGGTGTTGAGGGGCGGTGAGTGAAC
ACGCAAGCTGGGGGAACGGGCCCGGAAGGCTGCCGCCCTTCGCCAAGTTTCATCTAGGGTCG
CTGG

FIGURE 324

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142238

><subunit 1 of 1, 251 aa, 1 stop

><MW: 27954, pI: 9.22, NX(S/T): 1

MLGARLRLWVCAICSVCSMSVLRAYPNASPLLGSWSGGLIHLTYTATARNSYHLQIHKNGHVD
GAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNI FGSHYFDPENC RFQHQTLENGY
DVYHSPQYHFLVSLGRAKRAFLPGMNPYPYSQFLSRNEIPLIHFNTPIPRRHTRS AEDDSE
RDPLNLVKPRARMT PAPASCSQELPSAEDNSPMASDPLGVVRGGRVNT HAGGTGPEGCRPFA
KFI

Important features of the protein:**Signal peptide:**

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 175-179

N-myristoylation site.

amino acids 33-39, 100-106, 225-231, 229-235

HBGF/FGF family proteins

amino acids 73-124

GGAAAAGGTACCCGCGAGAGACAGCCAGCAGTCTCTGTGGAGCAGCGGTGGCCGGCTAGC**AT**
GGCTGTCTCTGGGGTCTGGCTCTGCCCTTTTCTTCTCTGCTGGGAGGTGGGGTCTCTGG
GAGCTCTGCAGGCCCCAGCACCCGACAGAGCAGACTGCGATGACAAACGACGACACAGAAG
TGCCCGCTATGACTCTAGCACCGGGCCACGCCGTCTGGAACTCAAACGCTGAGCGCTGAG
ACCTCTTCTAGGGCTCAACCCAGCCGGCCCCATTCCAGAAGCAGAGACCAGGGGAGCCAA
GAGAAATTTCCCTGCAAGAGAGACCAGGAGTTTCACAAAAAATCTCTCCAACTTCATGGTG
TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC
ACAGTTCAGACCATCACAGGCAGTGATCCCGAGGAAGCCATCTTTGACACCTTTGCACCCGA
TGACAGCTCTGAAGAGGCAAAGACACTCACAAATGGACATATTGACATTGGCTCACACCTCCA
CAGAAGCTAAGGGCCTGTCTCAGAGAGCAGTGCCCTCTTCCGACGGCCCCCATCCAGTCATC
ACCCCGTCAACGGGCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATACCCCC
GTCACGGGCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATACCCCCGTAT
GGTCCCCGGGATCTGATGTCACTTCTCTCGTGAAGCCCTTGTGACTGTCACAAACCTCAG
GTTATTAAATGCAGCATCAGAAATAGAAACAACAACCTTCAGCATCTCCGTGGGGCTCAGA
CATAGATCTCATCTCCACGGGAAGGGTGAAGGCTCTGTCACCTCCGATCCACCAGCTCTGC
CTAGACTCCACTGAAGCAAAACACACATCACTGAGGTACACAGCTCTGCCGAGACCTGTCC
ACAGCCGGCACCCAGAGTCAGCTGCACCTCATGCCACGGTTGGGACCCCACTCCCCACTAA
CAGCGCCACAGAAAGAGAAAGTGACAGCACCCGGGGCCACGACCTCAGTGGAGCTCTGGTCA
CAGTTAGCAGGAATCCCCTGGAAGAAACCTCAGCCCTCTCTGTTGAGACACCAAGTTACGTC
AAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGCTGGGTACGAGTGGGCAAAACAACCTC
CTTTGCTGGGAGCTCTGCTTCTCTTACAGCCCTCGGAAGCGCCCTCAAGAACTTCACCC
CTTCAGAGACCCGACCATGGACATGCACAACCAAGGGGCCCTTCCCCACCAGCAGGGACCTT
CTTCTTCTGTCTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACTTAGCCAA
GATCACAACTCAGCGAAGACCAGATGAAGCCCCAACAGCCACGCCACGACTGCCCGGAC
GAGGCCGACCACAGACCT**GA**AGTGCAGGTGAAAATGGAGGTTTCTCTCTCTGCGGCTGAGTG
TGGCTTCCCCGGAAGACCTCACTGACCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC
CGGGAACCTCACGCCCACGCGCTCACTTCCAGGTCTCTTACTGCGTGTGAGGAGAGGCTA
ACGGACATCAGCTGCAGCCAGGCATGTCCCGTATGCCAAAAGAGGGTGCTGCCCTAGCCTG
GGCCCCACCAGACAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG
AAGGGCAGCATGTCCAAGCCCCTAACCCAGATGTGGCAACAGGACCTCGCTCATCTCCAC
CGGAGTGTATGTATGGGAGGGGTTACCTGTTTCCAGAGGTGTCTTGGACTCACCTTGG
CAGATGTTCTGTGTTTCAGTAAAGAGAGACCTGATCACCCATCTGTGTGCTTCCATCCTGCA
TATAAATCTCACTAGTGTGGGCCAAAAAA

FIGURE 326

MGCLWGLALPLFFFCWEVGVSGSSAGPSTRADTAMTTDDTEVPAMTLAPGHALETQTL
 ETSSRASTPAGPIPEAETRGAKRISPAETRSFTKTSNFMVLIATSVETSAASGSPEGAGM
 TTVQTITGSDPEEAI FDTLCDDSSSEAKTLTMDILT LAHTSTEAKGLSSESSASSDGPHPV
 ITPSRASESSASSDGPHPVITPSRASESSASSDGPHPVITPSWSPGSDVTLLEALVTVTNI
 EVINCSITEIETTTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTEAKPHITEVTAETL
 STAGTTESAAPHATVGTPLPTNSATEREVTAPGATTL SGALVTVSRNPLEETSALSVETPSY
 VKVSGAAPVSI EAGSAVGKTSFAGSSASSYSPSEAALKNFTPSETPTMDIATKGPFPTSRD
 PLPSVPPTTTNSSRGTNSTLAKITTS AKTTMKPQQPRPRLPGRGRPQT

N-glycosylation sites:

amino acids 252-256, 445-449, 451-455

cAMP-and cGMP-dependent protein kinase phosphorylation site.

amino acids 84-90

Casein kinase II phosphorylation sites.

amino acids 37-41, 108-112, 131-135, 133-137, 148-152, 165-169,
 246-250, 254-258, 256-260, 269-273, 283-287, 333-337, 335-339,
 404-408, 414-418, 431-435

N-myristoylation sites.

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284, 314-
 320, 349-355, 386-392, 397-403, 449-455

ATP/GTP-binding site motif A (P-loop).

amino acids 385-393

FIGURE 327

GCGGAGCATCCGCTGCGGTCTCGCCGAGACCCCCGCGGGATTGCGCGGTCTTCCCGCGG
 GCGCGACAGAGCTGTCTCGCACCTGGATGGCAGCAGGGGCGCGGGGTCTCTCGACGCCA
 GAGAGAAATCTCATCTGTGACGCCCTTCTTAAAGCAAATAGACCAGAGGGGAGGATTAT
 CCTTGACCTTTGAAGACCAAACTAAACTGAAATTTAAATGCTTCTCGGGGAGAGGGGAG
 CTTGACTTACACTTTTGTAATAATTGCTTCCTGACACTAAGGCTGTCTGCTAGTCAGAATT
 GCCTCAAAAAGAGTCTAGAAGATGTTGTCTTACATCCAGTCATCTTCTTAAGGGAATC
 AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAAATTTCTGCTGTTCAAC
 AAAAAACATATCAGGGGACAAAGCATGTAACCTTGATGATCTTCGACACTCGAAAAACAGCTA
 GACAACCCAACCTGCTACCTATTTTCTGTCACGAGGAAGCCTGTCCATTGAAACACGCA
 AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG
 CCAAGAGTTACCCAGGAAGATTCTCTCTTACATGGCCAAATTTTCACAAAGCAGTCACTCCCC
 TAGCCCATCATCACACAGATTATTCAAAGCCCAACCGATATCTCATGGAGAGACACACTTTCT
 CAGAAGTTTGGATCCTCAGATCACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCA
 GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTACAATTTTCTCTGATCAAGAAA
 TAGCTCATCTGCTGCCTGAAATGTGAGTGCCTCCAGCTACGGTGGCAGTTGCTTCTCCA
 CATACCACCTCGGCTACTCCAAGCCCGCCACCTTCTACCCACCAATGCTTCAGTGACACC
 TTCTGGGACTTCCAGCCACAGCTGGCCACCACAGCTCCAGCTGTAACCACTGTCACTTCTC
 AGCCTCCCACGACCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATG
 GCTACACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA
 AACCATACCGTTTTACAGAAATCTCCAACCTAACTTTGAACACAGGGAATGTGTATAACCCTA
 CTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTCGGGAGGTT
 AGGGAGGCCAGTCCAGGCAGTTCTCCAGGGCAGTGTTCAGAAATCTCAGTACGGCTTCC
 ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTGTTTCTGGTGATAGGCC
 TCGTCTCTCTGGGTAGAATCCTTTGGAATCACTCCGAGGAAACGTTACTCAAGACTGGAT
 TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAACCTCGGTGTCTCTTAATTCATT
 TAGTAACCAAGCCCAATGCAATGAGTTTCTGCTGACTTGTCTAGTCTTAGCAGGAGGTTG
 TATTTTGAAGACAGGAAATGCCCCCTCTGCTTTCTCTTTTTTTTTTTGGAGACAGAGTCTT
 GCTCTGTTGCCAGGCTGGAGTGCAGTAGCAGATCTCGGCTCTCACCACAACCTCCGTCTC
 CTGGGTTCAAGCGATTCTCCTGCCTCAGCTCCTAAGTATCTGGGATTACAGGCATGTGCCA
 CCACACCTGGGTGATTTTGTATTTTAGTAGAGACGGGGTTTCAACATGTTGGTCAGGCTG
 GTCTCAAACTCCTGACCTAGTGATCCACCTCTCGGGCTCCCAAGTGCTGGGATTACAGG
 CATGAGCCACCACAGCTGGCCCCCTTCTGTTTATGTTTGGTTTTTGAGAAGGAATGAAGTG
 GGAACCAAAATTAGTAATTTTGGGTAATCTGTCTCTAAAATATTAGCTAAAAACAAAGCTCT
 ATGTAAGTAATAAAGTATAATTGCCATATAAATTTCAAATTTCAACTGGCTTTTATGCAAA
 GAAACAGGTTAGGACATCTAGGTTCCAATTCATTACATCTTGGTTCAGATAAAATCAAC
 TGTTTATATCAATTTCTAATGGATTGCTTTCTTTTATATGGATTCCTTTAAACCTTATT
 CCAGATGTAGTTCTTCCAATTAATATTGAATAAACTTTTGTACTCAA

FIGURE 328

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410

><subunit 1 of 1, 431 aa, 1 stop

><MW: 46810, pI: 6.45, NX(S/T): 6

MFFGGEGSLTYTLVLIICFLTLLRLSASQNCCLKKSLEDVVIDIQSSLKSGIRGNEPVYTSTQED
CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTFQAP
TDSKGSLETIPFTEISNLTNLNTGNVYNPTALSMNSVESSTMNKTSWEGREASPGSSSQGSV
PENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLLRRKRYSLDYLINGIYVDI

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

CTCCACCGGTGTCACGAGCCACAGA**ATG**CGGCCTCTGGTCTGCTATGGGGTTGGCTGCTGCT
CCCAGGTTTATGAAGCCTCGAGGGCCGACAGGAATACGGGGTTGCAAGGGGACAGTGTGT
CCCTGCAGTGCACCTACAGGAAGAGCTGAGGACCCAGGAAGTACTGTGTGCAGGAAGGTT
GGGATCTCTTCTCTCGCTGCTCTGGCACCATCTATGCAGAAAGCAAGGCCAGAGACAAAT
GAAGGGCAGGGGTGTCATCTCGTGACAGCCGCTCTCGCTTACTGTACCTTGTGAGTGA
ACCTTCACTTGCAGAACGCTGGGAGTACTGTGTGGGGTCGAAAACCGGGGCCGATGAG
TCTTTACTGATCTCTCTGTGTCTCTTCAGGCCCTGCTGTCTCCCTCCCTCTCTCCAC
CTTCCAGCCTCTGGCTACAACACGCTTGCAGCCCAAGCTGCAAAAGCTTACGAAACCAGCCG
CAGGATGTACTTCTCTGGGCTCTACCCGGCAGCCACCAGCCAAAGCAGGGGAAGACAGGG
GCTAGGCCCTCCATTTGCCAGGAGACTTCCGATCAGGGCAGCAAGAAAGCTTCTCAGTACAC
AGGAACCTCTCTTCAACCGAGGACTCTCTCTCTCGAGGAGCTCCGCCCCCTATGCGAGC
TGGACTCCACCTCAGCAGAGGACACCTGAGCTCTCAGCAGTGTGCTGCTCTAAGCCCGAG
GTGCTCATCCGATGGTCCGATACCTAGGCCAGTCTGTGTGTGCTGAGCCTTCTGTGACG
CGAGCCGCTGATGCCTTTCTGACGCCACTGTCTGTGTGGAGAAAGGAAGCTCAACAGGCCA
CGGAGACACAGAGAAGCAGAGAAGTTCTGGCTCTCAGCTTGACTGCGAGGAAAGGAAGCC
CCTTCCAGGCCCTGAGGGGACGTGATCTCATGCTTCCCTCCACCTCAGACCTCTGAGGAGG
CTGGGCTTCTCGAAGTTTGTCTAGCG**TAG**GGCAGGAGGCCCTCTGGCCAGCCGACCTGAT
GAAGCAGTATGGCTGGCTGGATCAGACCGGATTCGCCAAAGCTTCCACCTCAGGCCTCAGAG
TCCAGCTGCCGAGCTACCGGCTCTCCCACTCCCAAGCTCTCTCTTGCATGTTCCA
GCCTGACCTAGAAGCGTTTGTCAAGCCTGAGCCGACAGAGCGGTGGCTTGTCTTCCGGCTG
GAGACTGGGACCTCCGATAGGTTTCACTCCCTGGGCAGATACACAGCTGCTGACCTCA
CGAGGCCACAGCAAGGCTCAGTGGATCTGTGCTGAGTTTCAATCTGCCAGGAACCTCTGGGC
TCTATGCCAGTGTGCGGACCTGCTTCTTCTCCACTCAGACCCCACTTGTCTTCCCTCC
TGGCCTCTCAGACTAGTCCAGCTTCTGTGATCAGCTGGTGTGAAGAGGAGCATGTCT
GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACCTGCATCTCAGGCCCTTCAGGAAGCT
GTGAAAACCGTATTTCTGGCCGCCACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCG
GACTCTGAATCTAACAACTCCGAGTCACTGTGCGACTTGAAGTTGAGGGCCAGTGGGCCGTG
ATGAAGCTCTCAACCCCTTCACTTAGAGTCTGCAATTTGGGCTGTGACGCTCTCAACCTGCC
CAATAGCTCTGCTCTGTCTGCGACACAGATGACAGTGGGACTCCCTGAGGCCGTGCTAAG
TCCAGGCCCTTGGTCAGGTCAGGTGCACATTTGCAGGATAAGCCAGGACCGGCACAGAAGTGG
TTGCCCTTTNCAATTTGCCCTCCCTGNNCACTGCCTTCTTGCTTGGAAAAAATGATGAAGA
AAACCTTGGCTCTCTTGTCTGTAAGAGGTTACTGGCTATGGGTTCTGGTGGCTAGAGA
GAAAAGTAGAAAAACAGAGTGCAGTAGTGTCTTACACAGAGAGAGTAGAAACAGGCCGG
ATACCTGGAAGGTGACTCCGAGTCCAGCCCTCGAAGAGGGTCTGGGGGTTGGTGAAGTA
GCACAACACTATTTTTTTCTTTTCTTTCCATTATTATTGTTTTTAAGACAGAATCTCGTGCT
GCTGCCAGGCTGGAGTGCAGTGGAGCATCTGCAAACTCCGCCCTCTGGGTTCAAGTGATT
CTTCTGCTCAGCTCCCGAGTACGTTGGATTACAGGACGACACCAACCTGGCGTAATT
TTTGTACTTTTAGTAGAGATGGGGTTTACCATGTTGGCCAGGCTGGTCTTGAATCTCTGAC
CTCAAAATGAGCCTCTGCTTCACTCTCCCAATTTGCCGGGATTACAGGCTAGGCCACTGTG
TCTGGCCCTATTCTCTTAAAGAGTGAATTAAGAGTTGTCTAGTATGCAAACTTGGAAAG
ATGGAGAGGAAAAAGAAAGGAGAAACCAAAATGTCACCATATGCTCACCAGAGACTCATCAT
TATTTGTTTTTTGTTGATCTTCTTCCACTTTCTTCTTTCATCATATGTTGGCGGTGTTCTT
TTTACAGAGCAATTATCTGTATATACAACCTTTGTATCTCGCCTTTTCCACCTTATCGTTCC
ATCATCTTATTTCCAGCACTTCTCTGTGTTTACAGACCTTTTATAATAAAATGTTTCATCA
CGTGCATAAAAAAATAAAAAA

FIGURE 330

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLLVLLWGCLLLPGYEALGPEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS
 GTIYAE EEGQETMKGRVSIRDSRQELSLIVTLWNLTLDAGEYWC GVEKRGPD E S L L I S L F V
 FPGPCCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGAEPPLPG
 TSQYGHERTSQYTGTSPPHATSPPAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSI PMVRI
 LAPVLVLLSLLSAAGLIAFCSHLLLWRKEAQQATETQRNEKFWLSRLTAE EKEAPSQAPEGD
 VISMPPLHTSEELGFSKFVSA

Important features:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128